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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein – protein search, using sw model

June 28, 2001, 16:08:25; Search time 411.58 Seconds (without alignments) 4.500 Million cell updates/sec Run on:

US-09-724-406-24 90

1 DPPYGNPHYYAMDY 14 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

425026 seqs, 132305027 residues Searched:

425026 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL\_16:\* Database :

sp\_archea:\*
sp\_bacteria:\*
sp\_fungi:\*
sp\_human:\*

sp\_unclassified:\*
sp\_vertebrate:\*
sp\_virus:\* sp\_invertebrate:\*
sp\_mammal:\* sp\_organelle:\* sp\_phage:\* sp\_rodent:\* sp\_plant:\* sp\_mhc:\* 10:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           |        | Description     | O9m301 arabidopsis | 09kin9 myxococcus | Ognas7 homo sapien | 09hf59 ashbva goss | O9dab4 xenonis lae | 096185 plasmodium | Ognwa9 homosanien | 058076 pvrococciis | 041556 triticum ae | 09h710 homo sanien | Ognw41 homo sapien | Ognykg homo sapien |        | 11172 mm Still 24117 | ٠.     | 061230 Unitariigata C |        | Obsess loichneil | משמחומו הבישווומוזים | Q91428 alcaligenes |
|-----------|--------|-----------------|--------------------|-------------------|--------------------|--------------------|--------------------|-------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|----------------------|--------|-----------------------|--------|------------------|----------------------|--------------------|
| SUMMARIES |        | ΩI              | Q9M301             | Q9KJN9            | CSON60             | Q9HF59             | Q9DGB4             | 096185            | O9NWA9            | 058076             | 041556             | 09H7L0             | 09NW41             | O9NYK9             | Q9UFU7 | 09JL72               | 084688 | 061230                | O9KBNO | OGGBOR           | 000000               | 09L428             |
|           |        | DB              | 10                 | ~                 | 4                  | ٣                  | 13                 | Ŋ                 | 4                 | Н                  | 10                 | 4                  | 4                  | 4                  | 4      | 11                   | 7      | 'n                    | ~      | ľ                | 1 (                  | 7                  |
|           | •      | Match Length DB | 470                | 343               | 919                | 761                | 527                | 2573              | 276               | 329                | 381                | 484                | 614                | 855                | 878    | 938                  | 1080   | 2809                  | 497    | 553              | 1 0                  | 960                |
| ø         | Query  | Match           | 53.3               | 51.1              | 51.1               | 50.0               | 48.9               | 48.3              | 47.8              | 47.8               | 47.8               | 47.8               | 47.8               | 47.8               | 47.8   | 47.8                 | 47.8   | 47.8                  | 46.7   | 46.7             |                      | 40.7               |
|           |        | Score           | 48                 | 46                | 46                 | 45                 | 44                 | 43.5              | 43                | 43                 | 43                 | 43                 | 43                 | 43                 | 43     | 43                   | 43     | 43                    | 42     | 42               | 7                    | 7 +                |
|           | Result | . NO.           | 7                  | 7                 | 3                  | 4                  | S                  | 9                 | 7                 | 80                 | σ                  | 10                 | 11                 | 12                 | 13     | 14                   | 15     | 16                    | 17     | 18               | 10                   | <b>C</b> T         |

| O991y5 oryctolagus O86728 streptomyce O9pisl campylobact O988al pinus monti |                                  | 030220 ateles belz<br>006416 homo saplen<br>091940 paralichthy<br>020733 cenorhabdi |  | Q9y493 homo sapien O9xzb8 plasmodium O82036 petroselliuu O82037 petroselliuu O59551 pyrococcus Q38895 arabidopsis Q9sv94 arabidopsis |
|---|----------------------------------|---|--|--|
| 6 Q9GLY5<br>2 Q86728<br>2 Q9PIS1<br>10 Q9SBA1<br>5 Q17467                   | 00000                            | 7 Q30220<br>4 Q06416<br>8 Q9T9D0<br>5 Q20733  | 200000   | 4 09Y493<br>5 09X2B8<br>10 082036<br>10 082037<br>1 059551<br>10 038895  |
| 903<br>973<br>973<br>11 363<br>6 26<br>127                                  | 6 155<br>6 218<br>6 222<br>6 261 | 457<br>6 359<br>6 612<br>6 950<br>6 973   | 6 1194<br>6 1413<br>6 1590<br>6 1590<br>6 2197 |  |
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| 7 7 T   | <b>4444</b>                      | 4444  | 44444  | 411<br>40.5<br>40.5<br>40.5<br>40<br>40  |
| 20<br>22<br>23<br>24  | 25<br>27<br>28<br>28             | 3210  | 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8          | W 4 4 4 4 4 4 4 6 9 9 9 9 9 9 9 9 9 9 9 9  |

### ALIGNMENTS

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Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 12|
| SEQUENCE FROM N.A.
| SEQUENCE FROM N.A.
| SEQUENCE FROM N.A.
| Exablogasis sequencing project; | Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases. |
| Submitted (APR-2000) to the EMBL/GENBANK/DDBJ data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rieger M., Gabel C., Mueller-Auer S., Schaefer M., Zipp M., Mawes H.W., Rudd S., Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.;
Salanoubat M.; Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                          01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
HYPOTHETICAL 53.2 KDA PROTEIN.
                                                                                         470 AA
                                                                                              PRT;
                                                                                         PRELIMINARY;
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SEQUENCE FROM N.A.
                                                                                                                                    Q9M301;
                                                                                     Q9M301
RESULT
                                          Q9M301
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ö Gaps ; 0 Query Match 53.3%; Score 48; DB 10; Length 470; Best Local Similarity 63.6%; Pred. No. 13; Matches 7; Conservative 2; Mismatches 2; Indels 4 YGNPHYYAMDY 14 ò

83 YGLPYYYVLDY 93 qq

7 RESULT Q9KJN9 us-09-724-406-24.rspt

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[1]
SEQUENCE FROM N.A.
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                                                                                                                                           Cho K., Zusman D.R.; "Sporulation timing in Myxococcus xanthus is controlled by the espAB
                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Adams R.R., Eckley D.M., Mackay A., Earnshaw W.C.; "Characterization and expression of the human INCENP gene."; Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AF282265; AAF87584.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51.1%; Score 46; DB 4; Length 919; 66.7%; Pred. No. 55; tive 0; Mismatches 4; Indels
                                                                     Bacteria; Proteobacteria; delta subdivision; Myxobacteria; Myxococcales; Cystobacterineae; Myxococcaceae; Myxococcaceae
                                                                                                                                                                                                                                                                                  Length 343;
                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                              Cho K., Zusman D.R.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF163841; ARF87928.1; -.
Hypothetical protein.
SEQUENCE 343 AA; 36580 MW; 16E89C41B1023979 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             919 AA; 105536 MW; 8F93024E411087C6 CRC64;
                   01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
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Pred. No. 19;
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343 AA
                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
 PRT;
                                                                                                                                MEDLINE-20032045; PubMed-10564511;
                                                                                                                                                                        Mol. Microbiol. 34:714-725(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                INNER CENTROMERE PROTEIN INCENP.
                                                 HYPOTHETICAL 36.6 KDA PROTEIN.
                                                                                                                                                                                                                                                                                    51.1%;
77.8%;
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Best Local Similarity 77.8'
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 PRELIMINARY;
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                                                            Myxococcus xanthus.
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Best Local Similarity
Matches 8; Conserv
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281 PPYGEPPYY 289
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                                                                                         NCBI_TaxID=34;
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01-MAR-2001
                                                                                                                                                                                                       STRAIN-DZ2;
                                                                                                                       STRAIN-DZ2;
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Q9HF59;
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          Q9KJN9;
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ID Q9
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SEQUENCE FROM N.A.

Wendland J., Philippsen P.;

Hyphal morphogenesis is controlled by multiple Rho-protein modules in the filamentous ascomycete Ashbya gossypii.";

Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF210626; AAG41244.1;

SEQUENCE 761 AA, 86025 WW; C7334F46A06BB334 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
NCBI_TaxID=8355;
                                                                 Ashbya gossypii (Eremothecium gossypii).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Eremotheciaceae; Eremothecium.
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 53.8%; Score 44; DB 13; Length 527;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                Length 761;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Waga S., Sugino A.;
"Xenopus DNA polymerase epsilon subunit B.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL: AB448257; BAB12726.1; -
SEQUENCE 527 AA; 59688 WW; CF25EE4FB9C711C7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                           Score 45; DB 3;
Pred. No. 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  527 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA POLYMERASE EPSILON SUBUNIT B. POLE2.
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                                                                                                                                                                                                                                                                                                                                                                                                                50.0%;
77.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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Best Local Similarity
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628 PYGHPHYSA 636
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                                                                                                                                             NCBI_TaxID=33169;
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Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y., Yamamoto S., Sexine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y., Sakai M., Ogura K., Otsuka R., Nakazawa H., Takaniya M., Ohfuku Y., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K., Masuchi Y., Shizuya H., Kikuchi H.; "Complete sequence and gene organization of the genome of a hyperthermophilic archaebacterium, Pyrococcus horikoshii Or3."; DNA Res. 5:55-76(1998).
                      Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mikami K., Sakanoto A., Iwabuchi M.;
"The HBP-1 family of wheat basic/leucine zipper proteins interacts
with overlapping cis-acting hexamer motifs of plant histone genes.";
J. Biol. Chem. 269:9974-9985(1994).
-i- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Triticum destivum (Wheat).
Eukaryota, Viridiplantae, Embryophyta, Tracheophyta, Spermatophyta,
Magnoliophyta, Liliopsida, Poales, Poaceae, Pooideae, Triticeae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47.8%; Score 43; DB 1; Length 329;
61.5%; Pred. No. 52;
tive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (AUG-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37237 MW; 21485A787DB28294 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00338; BRLZ; I.
DNA-binding; Nuclear protein.
SEQUENCE 381 AA; 40683 MW; 448635628C15651F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-MAR-2001 (TrEMBLrel. 16, Last annotation update) TRANSCRIPTION FACTOR HBP-1A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; InterPro; InterPro; IPR002052; ...
Pfam: PF01170; UPF0020; 1.
PROSITE: PS00002; NG MTASE; UNKNOWN_1.
Hypothetical protein.
SEQUENCE 329 AA; 37237 WW; 21485A78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                           MEDLINE=98344137; PubMed=9679194;
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STRAIN-HOROSHIRIKOMUGI;
MEDLINE-94193693; Pubmed-8144592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00170; bZIP; 1.
PROSITE; PS00036; BZIP_BASIC; 1.
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Mendel; 15812; Triae; 2979; 15812.
InterPro; IPR001871; --
                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AP000002; BAA29412.1; -. InterPro; IPR000051; -.
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Matches 8; Conservative
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255 DPPYGNSTTLPMD 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000241
                                                                                                   SEQUENCE FROM N.A.
                                             NCBI_TaxID=53953;
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                                                                                                                                  STRAIN=OT3
                         Archaea;
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041556;
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A ISOGAL T., Cota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
A ISOGAL T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
A Nishikawa T., Nagal K., Sugano S., Shiratori A., Sudo H.,
A Madatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
A Matanaba S., Kimura K., Murakawa K., Ono Y., Takiguchi S.,
A Watanaba S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
A Ninomiya K., Iwayanagi T.;
A Ninomiya K., Iwayanagi T.;
A Ninomiya K., Iwayanagi T.;
B Ninomiya K., Iwayanagi M., Iway
MEDLINE-99021743; PubMed-9804551; Gardner M.J., Tettelin H., Carucci D.J., Cummings L.M., Aravind L., Koonin E.V., Shallom S., Mason T., Yu K., Fujil C., Pederson J., Shen K., Jing J., Aston C., Lai Z., Schwartz D.C., Pertea M., Salzberg S., Zhou L., Sutton G.G., Clayton R., White O., Smith H.O., Fraser C.M., Adams M.D., Venter J.C., Hoffman S.L.; "Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                           Score 43.5; DB 5; Length 2573;
Pred. No. 4.2e+02;
0; Mismatches 2; Indels 1.
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                                                                                                                                                                                                                    Science 282:1126-1132(1998).
EMBL; AE001396; AAC71881.1; -.
Hypothetical protein.
SEQUENCE 2573 AA; 308142 MW; 49E0D7E8967066CF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29622 MW; 8C96C7C5B41CD3A1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
HYPOPHETICAL 37.2 KDA PROTEIN PH0338.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              276 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequ
01-MAR-2001 (TrEMBLrel. 16, Last anno
HYPOTHETICAL 29, 6 KDA PROTEIN.
HOMO saplens (Human).
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Best Local Similarity 72.7'
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR01270; HDASUPER.
SEQUENCE 276 AA: 29622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 63.v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1436 DPEAYNNPHYY 1446
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RESULT Q9NWA9

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381 AA

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DB 10; Length 381;
47.8%; Score 43;
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RESULT 058076

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Query Match
Best Local Similarity
Matches 7; Conserv
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                                                                                                                                         Q9NYK9
                                                                                                                 RESULT 12
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Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.

BMBL, AR001190; BAA91545.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                  Gaps
                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                         Ohara O., Nagase T., Kikuno R., Okumura K.;
"The nucleotide sequence of a long cDNA clone isolated from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
CDNA FLJ10328 FIS, CLONE NT2RM2000588, WEAKLY SIMILAR TO HISTONE
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Pred. No. 80;
1; Mismatches 3; Indels
                  Indels
                                                                                                                                                                                                                                                                                                                                           Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases EMBL; -... AK024469; BAB15759.1; -...
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                                                                                                                                                                                                                                                                                                                                                                                    484 AA; 52327 MW; 1B1B0B363436A800 CRC64;
                                                                                                                                                      01-MAR-2001 (TrEMBLrel. 16, Created)
1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
FLJO0062 PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 614 AA.
                                                                                                                                484 AA
                  0; Mismatches
      Pred. No.
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                                                                                                                                PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                          47.8%;
   61.5%;
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                                                                                                                                 PRELIMINARY;
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                                         2 PPYGNPHYYAMDY 14
                                                                  77 PPYGTPPPYATMY 89
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298 DPPMGDPEYLA 308
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      Best Local Similarity
                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                TISSUE-SPLEEN;
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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Q9H7L0
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                  Matches
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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TISSUB-CERTYICAL CARCINOMA;

Li S., Fischle W., Verdin E., Walsh M.J.;

A novel class II HDAC is associated with the transcriptional homeodomain repressor CCAAT displacement protein.";

Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AF239243; AAF64491.1;

Interpro; IPR000286;

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Pfam, PF00850; HISL-Geacetyl; 1.

PFINITS; PR01270; HDASUPER.

SEQUENCE 855 AA; 92363 MW; 3157426AE1913DB6 CRC64;
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Pred. No. 1.5e+02;
1; Mismatches 3; Indels
47.8%; Score 43; DB 4; Length 614; 63.6%; Pred. No. 1e+02;
                                                                                 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
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                                                                                     1; Mismatches
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Matches 7; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-2000 (TrEMBLEEL 15,
01-0CT-2000 (TrEMBLEEL 15,
01-MAR-2001 (TrEMBLEEL 16,
HISTONE DEACETYLASE 7.
                                                                                 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                            428 DPPMGDPEYLA 438
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SEQUENCE
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STRAIN=D/UW-3-YCX;
MEDLINE=99000809; Pubmed=9784136;
Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-B6:C57BL/6;

MEDLINE-20107033, PubMed-10640276;

Rao H.Y., Downes M., Ordentlich P., Evans R.M.;

"Isolation of a novel histone deacetylase reveals that class I and deacetylases promote SMRT-mediated repression.";

Galss II deacetylases promote SMRT-mediated repression.";

EMBL; AF207749; AAF31419.1; -.

InterPro. IPR002086; -.

PRINTS; PR01270; HDASUPER.
                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Davis R.W.; "Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis.";
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             47.8%; Score 43; DB 4; Length 878; 63.6%; Pred. No. 1.5e+02; tive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Science 282:754-759(1998).
EMBL: AE001338: AAC68277.1; -.
Interpro: IPRO01460; -.
Pfam: PFC0905; Transpeptidase; 1.
SEQUENCE 1080 AA; 123959 WW; EE647FAB7FIFFEDD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 938 AA; 101318 MW; A282A36EBC840897 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NAY-2000 (TrEMBLrel. 13, Last annotation update)
PBP2-TRANSGLYCOLASE/TRANSPEPTIDASE.
                                                                                                                                                                                                                        01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
HISTONE DEACETYLASE 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chlamydia trachomatis.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID=013;
                                                                                                                                                                                            938 AA.
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Query Match
Best Local Similarity 63.vv
Best Local 7; Conservative
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753 DPPMGDPEYLA 763
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692 DPPMGDPEYLA 702
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                                                                              1 DPPYGNPHYYA 11
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      Query Match
      47.8%; Score 43; DB 2; Length 1080;

      Best Local Similarity 66.7%; Pred. No. 1.96+02;

      Matches 6; Consarvative 2; Mismatches 1; Indels 0; Gaps 0;

      Qy 1 DPPVGNPHY 9

      1 | 1|:1

      Db 662 EPPLGNPYY 670
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Search completed: June 28, 2001, 16:08:26 Job time: 954 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

June 28, 2001, 16:14:37; Search time 362.28 Seconds (Without alignments) 18.575 Million cell updates/sec

US-09-724-406-26

578 1 DIVLTQSPASLAVSLGQRAT......CQHSGELPFTFGSGTKLEIK Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

412676 seqs, 60623988 residues Searched:

412676 Potal number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

Database :

A\_Geneseq\_0601:\*

// SIDSB/gcgdata/geneseq/geneseqp/AA1982.DAT:\*
// SIDSB/gcgdata/geneseq/geneseqp/AA1982.DAT:\*
// SIDSB/gcgdata/geneseq/geneseqp/AA1982.DAT:\*
// SIDSB/gcgdata/geneseq/geneseqp/AA1985.DAT:\*
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/SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT:\*

SUMMARIES

Pred. No. Is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Anti-carcinoembryo Murine COLI VK cha VI region from an Murine Fd79 antibo Light chain variab Light chain variab Human thyroid stim Porphyrin antibody H. pylori HSP60-bi p12-k2. Synthetic Murine 206 antibod Description AAR80272 AAB69661 AAR15440 AAR60528 AAR75431 AAR52659 AAB10019 AAR28668 AAR85236 AAR60564 AAY39532 a DB Query Match Length 91.0 90.7 90.7 90.0 88.8 88.8 88.8 88.6 88.6 88.5 88.7 987.9 Score 526 524 521 520 513.5 513.5 512 510 510 509 508 Result No.

| Antibody variable Anti-human gp39 MA Mouse antibody F93 Mouse antibody F93 Mouse anti-diotyp Light chain variab Light chain variab Immunoglobulin L Antino acids sequen 31765 hybridoma VL N·terminal sequenc Monoclonal antibod Murine 340 Vl amin Murine 340 Vl amin Murine 340 Vl amin Murine anti-Fas an Anti-Fas ant Antibody 445 L cha Murine derived pro Immunoglobulin lig Anti-idiotype anti Immunoglobulin lig Anti-idiotype anti | ರ                |
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| AAB3510 AAW0372 AAR7545 AAR7545 AAW3773 AAW1957 AAW1957 AAW9054 AAW9089 AAW8611 AAR8610 AAW8611 AAR8708 AAW78186 AAY7816 AAY7816 AAY7896 AAY7896 AAY7896 AAY7896  | AAW345           |
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| 1128 88 7 94 1110111118 88 7 94 1110111118 88 111111111111111111111111  | 131              |
|   | ; <del>,</del> ; |
| 502.5<br>502.5<br>502.5<br>500.5<br>64.6<br>64.6<br>64.6<br>64.6<br>64.6<br>64.6<br>64.6<br>64  | 472              |
| 11111111111111111111111111111111111111  | 45               |

### ALIGNMENTS

AAR52659 standard; Protein; 212 AA. 16-JAN-1995 (first entry) AAR52659; AAR52659 RESULT 

Porphyrin antibody light chain.

Light; heavy; chain; monoclonal antibody; porphyrin; absorption spectrum; oxidase activity.

Mus musculus

JP06105686-A. 19-APR-1994. 92JP-0258584. 28-SEP-1992; 92JP-0258584. 28-SEP-1992;

(TOYM ) TOYOBO KK.

WPI; 1994-163128/20.

N-PSDB; AAQ62631.

Gene encoding mcnoclonal antibody against porphyrin - useful to produce antibody with modified properties, to interact with e.g.

Claim 4; Page 10-11; 16pp; Japanese.

P450, haemoglobin; etc.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Detecting infection by acid-fast microbes for diagnosis of Helicobacter pylori, comprises reacting a faecal sample with two binding reagents for antigens that survive intestinal passage
The sequences given in AAR52659-60 represent the light and heavy chains respectively of a monoclonal antibody which specifically recognises a specified porphyrin molecule. Using the genes encoding these proteins, the porphyrin antibody can be mass produced inexpensively. Features of the porphyrin monoclonal antibody may be modified, eg. absorption spectrum shift and expression of oxidase activity, by alterations within the coding region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Acid-resistant microorganism; detection; faecal; intestine; infection; monoclonal antibody; heat shock protein; HSP60; light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DIVLTQSPASLAVSLGQRATISCRASKSVSASGYNYMHWYQQKAGQPPKLLIHLASNLES 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                               Length 212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 GVPARFSGSGSGTDFTLNIHPVEEEDASTYYCQHSGELPFTFGSGTKLEIK 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lakner M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                            Score 526; DB 15;
Pred. No. 1.1e-37;
4; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Friedrichs U,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB10019 standard; Protein; 111 AA.
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                                                                                                                                                                                                                                                                                                                                                                            Query Match 91.0%;
Best Local Similarity 91.0%;
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98EP-0120517.
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                                                                                                                                                                                                                                                                             212 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ပဲ
                                                                                                                                                                                                                                                                                 Sequence
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at least one of the specified epitopes. The method is used to detect infection by acid-fast bacteria, particularly of the genera Helicobacter, whycobacterium and Campylobacter, specifically H. Pylori, H. hepaticus, M. tuberculosis, C. jejuni and C. pylori. (I) may also be used therapeutically. The method is direct and non-invasive, and provides an inexpensive and easily standardizable diagnosis, despite possible degradation of antigens during passage through the intestines. This sequence represents the H. pylori heat shock protein, HSP60-binding antibody (DMS ACC2356) light chain which is used to illustrate the method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, antibody, interleukin-6; receptor; IL-6R; light chain; L; H; heavy chain; variable region; mouse; monoclonal; hybridoma; AUK12-20; plasmid; pl2-k2; pl2-h2.
                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                          1 DIVLTQSPASLAVSLGQRATISCRASKSVSASGYNYMHWYQQKAGQPPKLLIHLASNLES 60
                                                                                                                                                                                                                                                                                         The sequences given in AAR28668-69 were encoded by plasmid sequences which were used in example to illustrate the production of a human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  has low antigenicity and contains mouse V-region complementarity determining regions
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                                                                                                                                                                                                                90.7%; Score 524; DB 21; Length 111; 90.1%; Pred. No. 8.4e-38;
                                                                                                                                                                                                                                                                                                                                     61 GVPARFSGSGSGTDFTLNIHPVEEEDASTYYCQHSGELPFTFGSGTKLEIK 111
                                                                                                                                                                                                                                                                                                                                                     Reconstituted human antibody to human interleukin-6 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tsuchiya M;
                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sato K,
                                                                                                                                                                                                                                              6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Mature peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Signal peptide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saldanha JW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR28668 standard; Protein; 131 AA.
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92JP-0032084.
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                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1992-398882/48.
                                                                                                                                                                                                                                Similarity
                                                                                                                                                                      111 AA;
                                                                                                                                         of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAQ30753.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-APR-1992;
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19-FEB-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAR-1993
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                                                                                                                                                                                                                                              Matches 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR28668;
                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide
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antibody which recognises human interleukin-6 receptor (IL-6R). The antibody comprises light (L) chain and heavy (H) chain variable regions which were derived from a mouse monoclonal antibody produced from the hybridoma AUK12-20 which contained the plasmids p12-k2 and
                                                                                                                                                   Gaps
                                                                                                                                                                        1 DIVLTQSPASLAVSLGQRATISCRASKSVSASGYNYMHWYQQKAGQPPKLLIHLASNLES 60
                                                                                                                                                                                    Varicella zoster virus gpIII antibody with humanised variable region - for treatment, prevention or diagnosis of varicella zoster virus infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antibodies (Ab) comprising a humanised variable region specifically binding to a varicella zoster virus (VZV) can be used to treat or bravent VZV infection. They may optionally be attached to a therapeutic agent. They may also be used, when labelled, to detect VZV particles and infected cells in blood; for the removal/
                                                                                                                                                                                                                                                                                                                                                                                                                           prevention;
MAb; mimetic;
                                                                                                                                                                                                                                                                                                                                                                                                                        Antibody; varicella zoster virus; Ab; VSV; treatment; prevention; infection; detection; isolation; monoclonal antibody; MAb; mimetic humanised; murine; heavy chain; light chain; variable region; CDR;
                                                                                                                                                   ó:
                                                                                                                    Score 521; DB 13; Length 131;
Pred. No. 1.8e-37;
4; Mismatches 7; Indels C
                                                                                                                                                                                                                          Murine 206 antibody variable light chain region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wallace TP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SCOT-) SCOTGEN BIOPHARMACEUTICALS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                  AAR85236 standard; Protein; 111 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 2; Figure 2; 58pp; English.
                                                                                                                                               4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24..38
/label= CDR 1.
54..60
/label= CDR 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Moss MT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93..101
/label- CDR 3.
                                                                                                                      90.1%;
90.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95WO-US05305
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                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Carr FJ, Harris WJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1996-010932/01.
                                                                                                                                   Similarity
                                                                                131 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAT06051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-APR-1995;
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                                                                                                                                  Best Local Sim
Matches 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NEWM; REI
                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                             AAR85236;
                                                                                                                      Query Match
                                                    p12-h2
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                                                                                                                                                                                                                                                                                                       AAR85236
                                                                                                                                                                                                                                                                                           RESULT
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neutralisation of infectious VZV in blood; for the selection/
isolation of human monoclonal Abs and for the design of (non-)
peptide mimetics with similar diagnostic and therapeutic uses. The
variable region CDR portion is derived from murine Ab 206 and the
heavy and light chain variable region frameworks are NEWM and REI
respectively. The framework may include at least one mutation that
improves binding specificity or affinity. The heavy and light chain
variable regions are preferably (VZVHu-VH, -VHKFIIS, -VHTLY,
                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                               1 DIVLTQSPASLAVSLGQRATISCRASKSVSASGYNYMHWYQQKAGQPPKLLIHLASNLES 60
                                                                                                                                                                                                                                                                                              AAQ71394 codes for AAR60564 the antibody light chain region of murine-human anti-carcinoembryonic antigen (CEA) chimeric antibody. Which can be used in in vitro immunoassays for the detection of CEA, and monitoring of tumour-associated antigen during therapy. It can also be used in vivo diagnostically, or in therapy for the treatment of tumours associated with colorectal and breast carcinomas, as well those of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for diagnosis
                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and therapy of carcinoma, e.g. breast or colorectal carcinoma
                                                                                                                                                                                                                                                                                                                                                               Length 111;
                                                                                                                                                                                                                                                                                                                                            61 GVPARFSGSGGTDFTLNIHPVEEEDASTYYCQHSGELPFTFGSGTKLEIK 111
                                                                                                                                                                                                                                               6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anti-carcinoembryonic antigen chimeric antibodies; CEAS; chimeric human-murine; breast or colorectal carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anti-carcinoembryonic antigen chimeric light chain Ab.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schlom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anti-carcinoembryonic antigen chimeric antibodies -
                                                                                                                                                                                                               90.0%; Score 520; DB 17; 91.0%; Pred. No. 1.8e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gastrointestinal tract, lung, ovary and pancreas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mezes PS, Rixon MW,
                                                                                                                                                                                                                                               4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (DOWC ) DOW CHEN CO.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR60564 standard; Protein; 110 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 11; Page 50; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94WO-US01709.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93US-0017570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                               Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gourlie BB, Kaplan DA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        muscaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chimeric Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1994-294331/36.
N-PSDB; AAQ71394.
                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                  Sequence 111 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chimeric Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-FEB-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-FEB-1993;
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Sequence

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61 GVPARFSGSGSGTDFTLNIHPVEEEDASTYYCQHSGELPFTFGSGTKLEIK 111

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                                                                                                                                                                                                                                                                                                                                                          Antibody; human; carcinoembryonic antigen; CEA; cancer; tumour imaging; tumour identification; metastasis; diagnosis; mouse; VK chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents the murine COL1 VK chain (COL1MuVK), and was
                                 Gaps
                                                                             1 DIVLTQSPASLAVSLGQRATISCRASKSVSASGYNYMHWYQQKAGQPPKLLIHLASNLES 60
                                1;
Length 110;
                                                                                                                                          61 gvparfsgsgsgtdftLnihpveeedaatyycqhsrelp-tfgggtkleik 110
                                                                                                                          61 GVPARFSGSGSGTDFTLNIHPVEEEDASTYYCQHSGELPFTFGSGTKLEIK 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New antibody specific for treatment and diagnosis of cancer
                                5; Indels
DB 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Harris WJ,
Score 513.5; DB 1
Pred. No. 6.5e-37;
                                5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carr FJ,
                                                                                                                                                                                                                                   AAY39532 standard; protein; 110 AA
                                                                                                                                                                                                                                                                                                                             Murine COL1 VK chain (COL1MuVK).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2; Fig 2; 82pp; English.
88.8%;
90.1%;
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                                                                                                                                                                                                                                                                                               (first entry)
                              Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anderson WHK, Tempest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       metabolic properties
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (DOWC ) DOW CHEM CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-550870/46.
                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 110 AA;
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                                                                                                                                                                                                                                                                                                                                                         Antibody;
                                                                                                                                                                                                                                                                AAY39532;
 Query Match
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antibody. Vectors which additionally contain genes encoding the human constant domains express a chimeric mouse-human antibody. The antibodies are useful in the detection and treatment of cancer. The chimeras should be less likely to cause anaphilaxis than the original murine antibody.
                                                                                                                                                                                                                      Antibody; heavy chain; light chain; variable region; cancer; mucin; hybridoma cell; murine; mouse; pancreatic cancer cell; expression vector; Fv; human; constant domain; chimera; anaphilaxis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The amino acid sequence of the variable region from the light chain of an antibody against cancer-specific mucin. The coding sequence was isolated from Nd2 hybridoma cells expressing a murine antibody reactive with pancreatic cancer cells. The DNA encoding the antibody variable regions from the heavy (AAQB9833) and light chains were isolated and incovectors. These vectors express the domains as an Evance incladed into vectors which additionally contain genes encoding the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New variable domains of antibody recognising cancer specific mucin - and related DNA and expression vectors, producing chimeric mouse-human antibody for diagnosis and treatment of cancer
Length 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 88.6%; Score 512; DB 16; Length 1: Best Local Similarity 87.4%; Pred. No. 8.9e-37; Matches 97; Conservative 7; Mismatches 7; Indels
                                                                                                                                                                                         VI region from an antibody against cancer-specific mucin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chung Y, Iba Y, Kaneko T, Sowa M, Yasukawa K;
                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "encoded by GAG"
                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                            AAR80272 standard; Protein; 112 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 6; Page 16-17; 25pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                   93..101
/label= CDR3
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/label= CDR2
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/label= CDR1
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                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference
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                                                                                                                                                             27-FEB-1996
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                                                                                                                                                                                                                                                                                          Synthetic.
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                                                                                                                                                                                                                                                                                                                                         Domain
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1 DIVLTQSPASLAVSLGQRATISCRASKSVSASGYNYMHWYQQKAGQPPKLLIHLASNLES 60

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1 divltqspasltvs1glratiscrasksvsasgysymhwyqqrpgqppklliylasnlqs 60

1 DIVLTQSPASLAVSLGQRATISCRASKSVSASGYNYMHWYQQRAGQPPKLLIHLASNLES 60

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Gaps

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5; Indels

5; Mismatches

Matches 100; Conservative

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Best Local Similarity

Query Match

88.8%; Score 513.5; DB 20; Length 110; 90.1%; Pred. No. 6.5e-37;

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                                                                                                                                                               NAME OF THE PROPERTY OF THE PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes a method of producing humanised immunoglobulins involving expressing in a cell a nucleic acid encoding a humanised version of an immunoglobulin. This is obtained by comparing a donor and human immunoglobulin and producing a combined antibody which contains part of each. These are useful in the treatment of graft-versus-host disease, transplant rejection, autoimmune diseases such as diabetes, rheumatoid arthritis, myasthenia gravis, multiple sclerosis and systemic lupus erythematosus, herpes infections, CMV virus infections demonstrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Humanised immunoglobulin; mouse; human; antibody; heavy chain; diabetes; light chain; graft versus host disease; transplant; autoimmune disease; multiple sclerosis; rheumatrid arthritis; systemic lupus erythematosus; myasthenia gravis; herpes infection; myeloid leukaemia; CWV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 divltqspaslavslggratiscrasksvttsdfsymhwyqqkpgqppklllylasnles 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Producing humanized immunoglobulin, involves producing a cell containing DNA segments encoding humanized heavy and light chain variable regions, and expressing the DNA segments in the cell -
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88.3%; Pred. No. 1.3e-36;
Live 3; Mismatches 10; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 GVPARFSGSGSGTDFTLNIHPVEEEDASTYYCQHSGELPFTFGSGTKLEIK 111
                                                                                                 Murine Fd79 antibody light chain SEQ ID NO: 46.
                                                                                                                                                                                                                                                                                            AAB69661 standard; Protein; 111 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 6; Fig 2; 145pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (PROT-) PROTEIN DESIGN LABS INC.
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89US-0310252.
90US-0590274.
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Matches 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Selick HE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-190856/19.
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                                                                                                                                                                                                                                                                                                                                                       AAB69661;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus sp.
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                                                                                                                                                                                                                                                  AAB69661
                                                                                                                                                                                                                             RESULT
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Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This is one of six antibody fragments from MAb's specific for domain 1 of ICAM-1. The peptide fragments can be used to treat or prevent rhinovirus infection. See AAR15437-R15443.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DIVLTQSPASLAVSLGQRATISCRASKSVSASGYNYMHWYQQRAGQPPKLLIHLASNLES 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          - can block
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Secretion sequence; vector; antibody; single chain antibody; promoter; Bacillus subtilis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Microbially expressed portions of monoclonal antibody - can attachment of rhinovirus ligands to inter-cellular adhesion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Light chain variable region of monoclonal antibody 5E8.
                                                                                                                                                                                                   HRV; ICAM-1; antigen-binding fragment; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sardana VV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 88.1%; Score 509; DB 12;
Best Local Similarity 87.4%; Pred. No. 1.8e-36;
Matches 97; Conservative 6; Mismatches 8;
                                                                                                                                                        Light chain variable region of MAb 2C2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tomassini JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR60528 standard; Protein; 111 AA.
                     AAR15440 standard; Protein; 125 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 20; 28pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                            91EP-0201243.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      90US-0532001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-APR-1995 (first entry)
                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Colonno RJ, Condra JH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MERI ) MERCK & CO INC
                                                                                                                                                                                                                           auto-immune disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1991-355850/49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       125 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       molecule (ICAM-1)
                                                                                                                                                                                                                                                                                                                                                                                                            25-MAY-1991;
                                                                                                             25-FEB-1992
                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-1990;
                                                                                                                                                                                                                                                                                                                                                                 04-DEC-1991
                                                                                                                                                                                                                                                                                                                 EP459577-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EP614982-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR60528;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                  AAR15440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR60528
ID AAR6
AAR15440
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WPI; 2001-032030/04.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DIVLTQSPASLAVSLGQRATISCRASKSVSASGYNYMHWYQQKAGQPPKLLIHLASNLES 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24..38
//note- "Complementarity determining region (CDR) 1"
/note- "CDR2"
                                                                                                                                        Vector for secretion of single chain antibody from Bacillus subtilis - contg. neutral protease promoter and specific leader sequence, providing high yield of soluble antibody for diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              thryoid stimulating hormone; TSH; human; variable region; heavy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human thyroid stimulating hormon antibody light chain variable.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 508; DB 15; Length 111; Pred. No. 1.9e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 GVPARFSGSGSGTDFTLNIHPVEEEDASTYYCQHSGELPFTFGSGTKLEI 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Indels
                                                                                       Tosi C;
                                                                                       Tortora O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Mismatches
                                                                                                                                                                                               Example 3; Figure 2; 27pp; English.
                                                                                       Grandi G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR75431 standard; Protein; 112 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chain; antibody; chimeric antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                        87.9%;
                     94EP-0200564.
                                          93IT-0MI0456.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              98; Conservative
                                                                                     Cuzzoni A, De FERRA F,
                                                                (ENIE ) ENIRICERCHE SPA
                                                                                                                                                                                                                                                                                                                                                                                      secretion in high yield
                                                                                                          WPI; 1994-281209/35
                                                                                                                                                                           therapeutic use
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                       N-PSDB; AAQ71286
                                          10-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
14-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR75431;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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recognising human thyroid stimulating hormone (hTSH). Prepr. of a chimeric antibody by expressing the DNA in a transformed host cell is also claimed. The anti-hTSH antibody has an additional useful function which could not be given by a mouse derived anti-TSH monoclonal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DIVLTQSPASLAVSLGQRATISCRASKSVSASGYNYMHWYQQKAGQPPKLLIHLASNLES 60
                                                                                                                                                                                                                                                                                                                                                           DNA encoding an antibody recognising human thyroid-stimulating hormone – and preparation of chimeric antibody by expressing the DNA in a transformed host cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence is the light chain variable region of an antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 GVPARFSGSGSGTDFTLNIHPVEEEDASTYYCQHSGELPFTFGSGTKLEIK 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 505; DB 16; Length 1
Pred. No. 3.5e-36;
7; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Filamentous phage; protein display; pVII; pIX; combinatorial antibody library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antibody variable region fusion protein #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Janda KD, Wirsching P, Lerner RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB35100 standard; Protein; 151 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 8; Fig 4; 8pp; Japanese.
93..101
/note= "CDR3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87.4%;
86.5%;
                                                                                                                                                                                                       93JP-0156707.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-MAY-2000; 2000WO-US14433.
                                                                                                                                                          93JP-0156707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SCRI ) SCRIPPS RES INST
                                                                                                                                                                                                                                                                                         WPI; 1995-220118/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                               (TOYJ ) TOSOH CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           112 AA;
                                                                                                                                                                                                                                                                                                                   N-PSDB; AAQ74148.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antibody (sic).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200071694-A1.
                                                                 JP07132097-A.
                                                                                                                                                        28-JUN-1993;
                                                                                                                                                                                                     28-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-MAY-1999;
                                                                                                              23-MAY-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-NOV-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB35100
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                                                                                                                           genome encoding a fusion protein. This fusion protein comprises an exogenous protein fused to the amino terminus of a filamentous phage pVII or pIX protein. This is useful in the design of proteins for medical, industrial, environmental and research applications.
                           polypeptide comprising exogenous polypeptide fused to amino terminus of pVII and pIX proteins, for constructing diverse heterodimeric polypeptide array
                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                 1 DIVLTQSPASLAVSLGQRATISCRASKSVSASGYNYMHWYQQKAGQPPKLLIHLASNLES 60
                                                                                                             The present invention describes a filamentous phage encapsulating a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Light chain; variable region; murine; mouse; anti-human; disease; glycoprotein 39; gp39; monoclonal; antibody; 39-1.7; hybridoma; diagnosis; inhibition; B-cell; activation; treatment; disorder; immune; autoimmune; allergic response; organ rejection; drug; graft versus host; cell imaging; tumour; targetted; delivery;
                                                                                                                                                                                                                                                                        1;
                                                                                                                                                                                                                                          Score 502.5; DB 22; Length 151;
Pred. No. 7.8e-36;
4; Mismatches 8; Indels 1;
             Novel filamentous phage encapsulating a genome encoding fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         113..121
/note= "complementarity determining region 3"
                                                                                                                                                                                                                                                                                                                                                                          /note= "complementarity determining region 2"
                                                                                                                                                                                                                                                                                                                                                           61 GVPARFSGSGSGTDFTLNIHPVEEEDASTYYCQHSGEL-PFTFGSGTKLEIK 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anti-human gp39 MAb 39-1.7 light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gordon ML;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gilliland LK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bajorath J, Gilliland LK
Hollenbaugh D, Siadak AW;
                                                                                  Example 1; Page 82-83; 90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label- mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW03723 standard; Protein; 132 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BRIM ) BRISTOL-MYERS SQUIBB CO.
                                                                                                                                                                                                                                         Query Match 86.9%;
Best Local Similarity 88.4%;
Matches 99; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96WO-US01119.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95US-0379057.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note=
                                                                                                                                                                                                  151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9623071-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aruffo AA,
Harris LJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     targeted.
                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW03723;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide
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The present sequence is the light chain variable region of the murine anti-human glycoprotein (gp) 39 monoclonal antibody (MAb) can member of the murine kappa II subfamily). The MAb was prepd. by immunising a 6-8 week old BALB/c mouse with a gp39-CD8 fusion protein, and 3 days later harvesting and fusing spleen and lymph cells to mouse melanoma cells, to produce an anti-human gp39 MAb producing hybridoma. The MAb may be useful for diagnosing disease states, inhibiting B-cell activation and for treating immunological disorders, e.g. autoimmune disorders, allergic responses, organ rejection and graft versus host disease. It may also be used for imaging cells which express gp39 on their surface, e.g. tumour cells, and to target therapeutic agents to such cells. The MAb inhibits the CD40/gp39 interaction, therefore limiting both prim and sec. responses to T-cell dependent antigens and Ab prodn. Specific to these antigens. A typical compsn. for intramuscular injection pref. contains 50 mg of MAb in 1 ml of sterile buffered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Primer; amplification; PCR; mouse; kappa chain; heavy chain; Fab; antibody; immunotolerance; animal; variegated display library; variable region; antipoen; immunorecessive; cell surface marker; foetal; cancer; stem cell; variant; therapy; Alzheimer's disease; hybridoma; familial hypercholesterolaemia; binding affinity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DIVLTQSPASLAVSLGQRATISCRASKSVSASGYNYMHWYQQRAGQPPKLLIHLASNLES 60
                                                                Monoclonal antibodies specific for different epitope(s) on human gp39 - used for inhibiting B cell activation and for the diagnosis of various disorders, e.g. cancer, psoriasis etc..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse antibody F33-2 light chain variable region protein sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 GVPARFSGSGSGTDFTLNIHPVEEEDASTYYCQHSGELPFTFGSGTKLEIK 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 502; DB 17;
Pred. No. 7.5e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR75457 standard; Protein; 218 AA
                                                                                                                                           Claim 93; Fig 7A; 167pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86.9%;
86.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94WO-US14106.
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93US-0164022.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-FEB-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 86.5 es 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GENZ ) GENZYME CORP
             WPI; 1996-362694,/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 132 AN;
                                  N-PSDB; AAT35975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9515982-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-DEC-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR75457;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR75457
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The sequence of the light chain variable region from the mouse antibody FB3-2. This sequence was isolated from a variegated display library (VDL) of variable regions derived from a repertoire of antibodies from an immunotolerised animal. The VDL is generated by PCR amplifying the variable regions from the antibody coding sequences using the primers AAQ74153-74. The variable regions, esp the complementarity determining regions (CDRs) see AAR7462-93 for examples of CDRs) from the immunotolerant animals' antibodies are used to construct an antibody against a immunorecessive antigon e.g. a cell surface marker on a foetal, against a immunorecessive antigon e.g. acell surface marker on a foetal, cancer or stem cell, which can differentiate between variant or related forms of the antibodies generated can be used in the diagnosis, e.g. detection of the immunorecessive antigen, or in therapy e.g. of cancer, Alzheimer's disease or familial hypercholesterolaemia. The method of production of the antibody allows rapid and sensitive isolation of antibodies that would be difficult to isolate by standard methods. The antibodies produced have greater binding affinity than the contract of the methods.
                                                                                                                           Generating new antibodies specific for immunorecessive epitopes by selection from variegated V gene library cloned from immuno:tolerance derived antibody repertoire, useful in diagnosis,
  Copeland DP, Hillhouse D, Johnson T;
                                                                                                                                                                                                                                                                     Disclosure; Page 76-77; 109pp; English.
                                                                                                                                                                                                                 purifcn. and therapy, e.g. of cancer
                                              WPI; 1995-224291/29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  218 AA;
                                                                               N-PSDB; AAQ92501
     Barsomian G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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0; Gaps 86.5%; Score 500; DB 16; Length 218; 84.7%; Pred. No. 1.9e-35; ive 7; Mismatches 10; Indels 94; Conservative Best Local Similarity Query Match Matches

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1 DIVLTQSPASLAVSLGQRATISCRASKSVSASGYNYMHWYQQKAGQPPKLLIHLASNLES 60 g ò ŏ

61 GVPARFSGSGSGTDFTLNIHPVEEEDASTYYCQHSGELPFTFGSGTKLEIK 111 

AAR75459 standard; Protein; 218 AA 07-FEB-1996 (first entry) AAR75459; 

Mouse antibody F4-7 light chain variable region protein sequence

Primer; amplification; PCR; mouse; kappa chain; heavy chain; Fab; antibody; immunotolerance; animal; variegated display library; variable region; antigen; immunorecessive; cell surface marker; foetal; cancer; stem cell; variant; therapy; Alzheimer's disease; hybridoma; familial hypercholesterolaemia; binding affinity.

Mus musculus.

WO9515982-A2

15-JUN-1995.

94WO-US14106 08-DEC-1994; 94US-0350400. 93US-0164022. 06-DEC-1994; 08-DEC-1993;

The sequence was isolated from a variegated display library (VDL) of variable regions derived from a repertoire of antibodies from an immunoclerised animal. The VDL is generated by PCR amplifying the cimmunoclerised animal. The VDL is generated by PCR amplifying the variable regions from the antibody coding sequences using the primers AAQ74153-74. The variable regions, esp the complementarity determining regions (CDR; see AAR75462-93 for examples of CDRs) from the immunoclerant animals' antibodies are used to construct an antibody against a immunocrecessive antigen e.g. a cell surface marker on a foetal, cancer or stem cell, which can differentiate between variant or related diagnosis, e.g. detection of the immunorecessive antigen, or in therapy e.g. of cancer, Alzheimer's disease or familial hypercholesterolaemia. The method of production of the antibody allows rapid and sensitive isolation of antibodies that would be difficult to isolate by standard methods. The antibodies produced have greater binding affinity than those produced by combinatorial/hybridoma methods. sequence of the light chain variable region from the mouse antibody by selection from variegated V gene library cloned from immuno:tolerance derived antibody repertoire, useful in diagnosis, Senerating new antibodies specific for immunorecessive epitopes Indels Copeland DP, Hillhouse D, Johnson T; 10; 7; Mismatches Disclosure; Page 80-81; 109pp; English. purifcn. and therapy, e.g. of cancer Best Local Similarity 84.7 Matches 94; Conservative (GENZ ) GENZYME CORP. WPI; 1995-224291/29. N-PSDB; AAQ92503 Barsomian G, Seguence Query Match g

Gaps ö 86.5%; Score 500; DB 16; Length 218; 84.7%; Pred. No. 1.9e-35;

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1 DIVLTQSPASLAVSLGQRATISCRASKSVSASGYNYMHWYQQRAGQPPKLLIHLASNLES 60

61 GVPARFSGSGSGTDFTLNIHPVEEEDASTYYCQHSGELPFTFGSGTKLEIK 111

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Search completed: June 28, 2001, 16:14:38 Job time: 1326 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

June 28, 2001, 16:01:15; Search time 138.34 Seconds (without alignments) 16.163 Million cell updates/sec Run on:

US-09-724-406-26

Perfect score: Sequence:

578 1 DIVLTQSPASLAVSLGQRAT......CQHSGELPFTFGSGTKLEIK 111 Scoring table:

193259 seqs, 20144635 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: /cgn2\_6/ptcdata/2/laa/5A\_COMB.pep:\*
2: /cgn2\_6/ptcdata/2/laa/5B\_COMB.pep:\*
3: /cgn2\_6/ptcdata/2/laa/6A\_COMB.pep:\*
4: /cgn2\_6/ptcdata/2/laa/6B\_COMB.pep:\*
5: /cgn2\_6/ptcdata/2/laa/pcTUS\_COMB.pep:\*
6: /cgn2\_6/ptcdata/2/laa/pcTUS\_COMB.pep:\* Issued\_Patents\_AA:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | Description    | Sequence 25, Appl | 25.              |                 | 'n              |                  | 46               | 46,              | 46,              | 46,              | Sequence 46, Appl | 4, 4             | 53,               | 16,              | 57,               |                   | 20,               | 7               | 7               | ω,              | Sequence 14, Appl | 'n              | 9               |                 | ω,              | 26.              | 26,              | 26,               |
|-----------|----------------|-------------------|------------------|-----------------|-----------------|------------------|------------------|------------------|------------------|------------------|-------------------|------------------|-------------------|------------------|-------------------|-------------------|-------------------|-----------------|-----------------|-----------------|-------------------|-----------------|-----------------|-----------------|-----------------|------------------|------------------|-------------------|
| SUMMARIES | ΩI             | US-08-137-117D-25 | US-08-436-717-25 | US-08-017-570-2 | US-08-471-426-2 | PCT-US94-01709-2 | US-07-634-278-46 | US-08-477-728-46 | US-08-474-040-46 | US-08-487-200-46 | US-08-484-537-46  | US-08-207-169A-4 | PCT-US94-14106-53 | US-08-379-057-16 | PCT-US94-14106-57 | US-08-653-402B-12 | US-08-483-749A-20 | US-08-483-636-2 | US-08-483-632-2 | US-08-491-845-8 | US-08-579-378A-14 | US-08-589-939-3 | US-08-466-151-6 | US-08-442-542-8 | US-08-765-469-8 | US-08-111-080-26 | US-08-211-980-26 | PCT-US93-07967-26 |
|           | DB             |                   | 7                | Н               | -               | 2                | П                | Н                | ٦                | -                | 4                 | ~                | S                 | ~                | Ŋ                 | 7                 | ٣                 | 7               | 7               | _               | 4                 | ო               | m               | Н               | m               | Н                | -                | 2                 |
|           | Length         | 131               | 131              | 110             | 110             | 110              | 111              | 111              | 111              | 111              | 111               | 111              | 111               | 132              | 218               | 146               | 110               | 132             | 132             | 111             | 131               | 131             | 106             | 110             | 110             | 120              | 120              | 120               |
| ф         | Query<br>Match | 90.1              | 90.1             | 88.8            | 88.8            | 88.8             | 88.2             | 88.2             | 88.3             | 88.2             | 88.2              | 87.9             | 87.4              | 86.9             | 86.5              | 84.7              | 83.8              | 82.9            | 82.9            | 82.2            | 82.0              | 81.7            | 79.8            | 79.7            | 79.7            | 78.4             | 78.4             | 78.4              |
|           | Score          | 521               | 521              | 513.5           | 513.5           | 513.5            | 510              | 510              | 510              | 210              | 510               | 208              | 505               | 502              | 200               | 489.5             | 484.5             | 479             | 479             | 475             | 474               | 472             | 461             | 460.5           | 460.5           | 453              | 453              | 453               |
|           | Result<br>No.  |                   | 7                | æ               | 4               | 'n               | φ.               | 7                | Φ.               | on ;             | 10                | 11               | 12                | 13               | 14                | 15                | 16                | 17              | 18              | 19              | 20                | 21              | 22              | 23              | 24              | 25               | 26               | 27                |

amino acid

| Appl             | Appl             | Appli           | Appl             | Appl             | Appl              | Appl             | Appl             | Appl              | Appl             | Appl             | Appl             | Appl             | Appl             | Appl             | Appl             | Appl             | Appl             |  |
|------------------|------------------|-----------------|------------------|------------------|-------------------|------------------|------------------|-------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|--|
| 18,              | Ξ                | 7               | 22               | 22               | 22,               | 24,              | 24,              | 24,               | 54,              | 54,              | 54,              | 54,              | 54,              | 67.              | 67,              | 67,              | 67,              |  |
| Sequence         | Sequence         | Sequence        | Sequence         | Sequence         | Sequence          | Sequence         | Sequence         | Sequence          | Sequence         | Sequence         | Sequence         | Sequence         | Sequence         | Sequence         | Sequence         | Sequence         | Sequence         |  |
| US-08-888-366-18 | US-08-275-053-11 | US-08-466-151-2 | US-08-111-080-22 | US-08-211-980-22 | PCT-US93-07967-22 | US-08-111-080-24 | US-08-211-980-24 | PCT-US93-07967-24 | US-07-634-278-54 | US-08-477-728-54 | US-08-474-040-54 | US-08-487-200-54 | US-08-484-537-54 | US-07-634-278-67 | US-08-477-728-67 | US-08-474-040-67 | US-08-487-200-67 |  |
| a                | Н                | ٣               | -                | ٦                | S                 |                  | -                | Z                 | Н                | ч                | Н                | ч                | 4                | ~                | -                | Н                | П                |  |
| 112              | 111              | 111             | 121              | 121              | 121               | 120              | 120              | 120               | 111              | 111              | 111              | 111              | 111              | 131              | 131              | 131              | 131              |  |
| 78.3             | 77.9             | 77.9            | 77.9             | 77.9             | 77.9              | 77.3             | 77.3             | 77.3              | 77.2             | 77.2             | 77.2             | 77.2             | 77.2             | 77.2             | 77.2             | 77.2             | 77.3             |  |
| 452.5            | 450              | 450             | 450              | 450              | 450               | 447              | 447              | 447               | 446              | 446              | 446              | 446              | 446              | 446              | 446              | 446              | 446              |  |
| 28               | 29               | 30              | 31               | 32               | 33                | 34               | 35               | 36                | 37               | 38               | 39               | 40               | 41               | 42               | 43               | 44               | 45               |  |
|                  |                  |                 |                  |                  |                   |                  |                  |                   |                  |                  |                  |                  |                  |                  |                  |                  |                  |  |

### ALIGNMENTS

```
Sequence 25 Application US/08137117D
Fater No. 5795965
GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: BENDIG, Mary
APPLICANT: BENDIG, Mary
APPLICANT: GATO, Koh
APPLICANT: SATO, Koh
APPLICANT: MARY
APPLICANT: SATO, Koh
APPLICANT: SATO, Koh
APPLICANT: MARY
APPLICANT: SATO, Koh
APPLICANT: ADDRESS:
ADDRESSEE: FOLEY & Lardner
ADDRESSEE: FOLEY & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY USA
ZIP: Z0007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117D
FILING DATE: 20-DEC-1993
CLASSIFICATION: SAME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: JOAN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGSER, MARION:
NAME: WEGSER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53466/126/AAOK
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3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 534
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFRAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 904136
INFORMATION FOR SEQ ID NO: 25:
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CITY: Washington
US-08-137-117D-25
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RESULT
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                                                                                                                                            0; Gaps
                                                                                                                                                                                                          21 DIVLIQSPASLGVSLGGRATISCRASKSVSTSGYSYMHWYQQKPGQTPKLLIYLASNLES 80
                                                                                                                                                                                    1 DIVLTQSPASLAVSLGQRATISCRASKSVSASGYNYMHWYQQRAGQPPKLLIHLASNLES 60
                                                                                                                                                                                                                                                                       61 GVPARFSGSGSGTDFTLNIHPVEEEDASTYYCQHSGELPFTFGSGTKLEIK 111
                                                                                                                                                                                                                                                                                             Score 521; DB 1; Length 131;
Pred. No. 6.1e-48;
4; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: SATO, Koh
APPLICANT: BENDIG, Wary
APPLICANT: BENDIG, Wary
APPLICANT: SALDANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIC CATON: 536
PRIOR APPLICATION: 536
APPLICATION NUMBER: US/08/137,117
FILLING DATE: 20-DEC-1993
APPLICATION NUMBER: WO PCT/JP92/00544
FILLING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-32084
FILLING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-95476
FILLING DATE: 27-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, HATOld C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 53466/126/AAOK TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Foley & Larunca
STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/436,717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 25, Application US/08436717
Patent No. 5817790
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25,258
                                                                                                  90.1%;
90.1%;
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(202)672-5399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: WEGNER, Harold C. REGISTRATION NUMBER: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                      Best Local Similarity 90.1
Matches 100; Conservative
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; MOLECULE TYPE: protein
US-08-436-717-25
               ; MOLECULE TYPE: protein US-08-137-117D-25
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TOPOLOGY: linear
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20007-5109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DIVLTQSPASLAVSLGQRATISCRASKSVSASGYNYMHWYQQKAGQPPKLLIHLASNLES 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 88.8%; Score 513.5; DB 1; Length 110; Best Local Similarity 90.1%; Pred. No. 3.1e-47; Matches 100; Conservative 5; Mismatches 5; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: RIXON, MARK W
APPLICANT: MEZES, PETER S
APPLICANT: RAPLAN, DONALD A
APPLICANT: SCHLOM, JEFFREY
TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 GVPARFSGSGSGTDFTLNIHPVEEEDASTYYCQHSGELPFTFGSGTKLEIK 111
                                                                                                                                                                 61 GYPARFSGSGSGTDFTLNIHPVEEEDASTYYCQHSGELPFTFGSGTKLEIK 111
                                                                                                                                                                                      Score 521; DB 2; Length 131;
Pred. No. 6.1e-48;
4; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/017,570
FILING DATE: 19930216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY AGENT INFORMATION:
NAME: ULMER, DUANE C
REGIGTRATION NUMBER: 34,941
REFERENCE/DOCKET NUMBER: C-38,777
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                         ; Sequence 2, Application US/08017570 ; Patent No. 5472693
                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: GOURLIE, BRIAN B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Duane C. Ulmer STREET: P.O. Box 1967 CITY: Midland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (517) 636-8104 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
  90.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     110 amino acids
                                            Matches 100; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    424
    Query Match
Best Local Similarity
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                       RESULT 3
US-08-017-570-2
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COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

88.8%; Score 513.5; DB 1; Length 110;
Best Local Similarity 90.1%; Pred. No. 3.1e-47;
Matches 100; Conservative 5; Mismatches 5; Indels 1
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GENERAL INFORMATION:
APPLICANT: THE DOW CHEMICAL COMPANY
APPLICANT: THE DOW CHEMICAL COMPANY
APPLICANT: U.S.A. DEPT. OF HEALTH AND HUMAN SERVICES
TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Duane C. Ulmer
STREET: P.O. Box 1967
CITY: Midland
                                                                                                                  APPLICANT: RIXON, MARK WAS APPLICANT: RESS, PETER S
APPLICANT: REPLAN, DONALD A
APPLICANT: SCHLOM, JEFREY
APPLICANT: SCHLOM, JEFREY
TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
NUMBER OF SEQUENCES: 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUW TYEE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTLIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,426
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION NUMBER: 08/017,570
FILING DATE: 16-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAMME: ULANE, DUAME C
REGISTRECOMMUNICATION NUMBER: C-38,777
TELECOMMUNICATION SEQ ID NO: 2:
CFONTENTER CHARRACTERISTICS:
                  Sequence 2, Application US/08471426 Patent No. 5808033 GENERAL INFORMATION: APPLICANT: GOURLIE, BRIAN B
                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Duane C. Ulmer
STREET: P.O. Box 1967
CITY: Midland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: protein US-08-471-426-2
                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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US-08-471-426-2
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STATE:
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1; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 5; Length 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 GVPARFSGSGSGTDFTLNIHPVEEEDASTYYCQHSGELPFTFGSGTKLEIK 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 GVPARFSGSGSGTDFTLNIHPHEEDAATYYCQHSRELP-TFGGGTKLEIK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 513.5; DB 5; Leuy... -
Pred. No. 3.1e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-07-634-278-46

| Sequence 46, Application US/07634278
| Sequence 46, Application US/07634278
| Patent No. 5530101
| GENERAL INFORMATION:
| APPLICANT: QUEEN, Cary L. APPLICANT: CO, Man Sung
| APPLICANT: CO, Man Sung
| APPLICANT: COELINGH, Kathleen L. APPLICANT: COELINGH, Kathleen L. APPLICANT: COELINGH, Kathleen L. APPLICANT: SELICK, Harold E. TITLE OF INVENTON: IMPROVED HUMANIZED IMMUNOCLOBLINS NUMBER OF SEQUENCES: 113
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: Transend and Townsend Khourie and Crew STREET: 379 Lytton Avenue
                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/01709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SCFWARE: Patentin Release #1.0, Version #1.25 SCFWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278 FILING DATE: 19-DEC 1990 CLASSIFICATION: 424 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274 FILING DATE: 28-SEP-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88.8%; Scor.
90.1%; Pred. No. 5...
5; Mismatches
                                                                                                                                                                                                                                                                                                             38,777-F
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COMPUTER: IBM. PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: ULMER, DUANE C
REGISTRATION NUMBER: 34,941
REFERENCE/DOCKET NUMBER: 38,7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 636-8104
ZIP: 48641-1967
COMPUTER READABLE FORM:
MEDIUM TYPE: Eloppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (517) 636-8104 INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: protein PCT-US94-01709-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA: APPLICATION NUMBER: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
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STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                       FILING DATE:
CLASSIFICATION:
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us-09-724-406-26.rai

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DIVLTQSPASLAVSLGQRATISCRASKSVSASGYNYMHWYQQKAGQPPKLLIHLASNLES 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DIVLTQSPASLAVSLGQRATISCRASQSVSTSTYNYMHWYQQRPGQPPKLLIKYASNLES 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GVPARFSGSGFGTDFTLNIHPVEEEDTVTYYCQHSWEIPYTFGGGTKLEIK 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 GVPARFSGSGSGTDFTLNIHPVEEEDASTYYCQHSGELPFTFGSGTKLEIK 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88.2%; Score 510; DB 1; Length 111; 88.3%; Pred. No. 7.2e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: QUEEN, Cary L.
APPLICANT: SCHEEDEK, William P.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNGELOBLINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLIM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patent PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,728
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Mismatches
                                                                                                                                                                        11823-002600
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY,AGENT INFORMATION:
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 46, Application US/08477728
Patent No. 5585089
GENERAL INFORMATION:
                                                                                                              NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFRENCE/DOCKET NUMBER: 1182:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2420
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
STRANDENESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 88,33
Matches 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-07-634-278-46
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Palo Alto
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 GVPARFSGSGSGTDFTLNIHPVEEEDASTYYCQHSGELPFTFGSGTKLEIK 111
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                                                                                                                                                                                                                                                                                                                                                                                                    88.2%; Score 510; DB 1; Length 111; illarity 88.3%; Pred. No. 7.2e-47; Conservative 3; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:

APPLICANT: QUEEN, Cary L.

APPLICANT: CO, Man Sund

APPLICANT: CO, Man Sund

APPLICANT: CANDELDER, William P.

APPLICANT: CALINGH, Rathleen L.

APPLICANT: SELICK, Harold E.

TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS

NUMBER OF SEQUENCES: 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,040
FILING DATE: OF-JUN-1995
CLASSIFICATION: 536
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                                               11823-002600
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FILING DATE: 07-JUN 10.1
FILING DATE: 07-JUN 10.1
APPLICATION UNMBER: US 07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US 07/290,975
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 46, Application US/08474040; Patent No. 5693761
             REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
RECISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Townsencements: 379 Lytton Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 13-FEB-1989 PRIOR APPLICATION DATA:
                                                                                                                                                                                                    LENGTH: 111 amino acids
Smith, William M
                                                                                                                                                                                                                                                      single
                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 98; Conserva
                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94301
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US-08-474-040-46
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                          1 DIVLTQSPASLAVSLGQRATISCRASKSVSASGYNYMHWYQQKAGQPPKLLIHLASNLES 60
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                                                                                                                                                                                                                                                                                                                                 Ouery Match

88.2%; Score 510; DB 1; Length 111;
Best Local Similarity 88.3%; Pred. No. 7.2e-47;
Matches 98; Conservative 3; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHWEIDER, William P.
APPLICANT: SCHWEIDER, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
APPLICANT: SELICK, Harold E.
APPLICANT: SELICK, HAROVED HUMANIZED IMMUNOGLOBLINS NUMBER OF INVENTION: 113
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,200
FILING DATE: 7-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Townsend and Townsend and Crew 379 Lytton Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AFTILING DATE: 10,108,481,200
CLASSIFICATION: 424
PRIOR APPLICATION 1995
FILING PAPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William N
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002610
TELECOMMUNICATION INFORMATION:
THE PROMINE: ALL NUMBER: 130,233
REFERENCE/DOCKET NUMBER: 130,233
THE PROMINE: ALL NUMBER: 130,233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 9
US-08-487-200-46
; Sequence 46, Application US/08487200
; Patent No. 5693762
; GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
                        TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
STRANDEDNESS: single
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (415) 326-2400
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                                                                                                                                                                                                      ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-474-040-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
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CITY: Palo Alto
STATE: California
COUNTRY: US
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GVPARFSGSGSGTDFTLNIHPVEEEDASTYYCQHSGELPFTFGSGTKLEIK 111
                                                                                                                                                                                                                                                         88.2%; Score 510; DB 1; Length 111; 88.3%; Pred. No. 7.2e-47;
                                                                                                                                                                                                                                                                                                       10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELLNGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
CORRESPONDENCE: 113
CORRESPONDENCE: ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: 379 Lytton Avenue CITY: Palo Alto STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAT-entin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,537
                                                                                                                                                                                                                                                                                                       3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 11823-002600 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 18-DEC-1988
ATTORNEY/AGGET INFORMATION:
NAME: SMITH MAILIAM M
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 46, Application US/08484537
; Patent No. 6180370
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 46:
                                           SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
  TELEFAX: (415) 326-2422 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: QUEEN, Cary L.
                                                                                                                                                                                                                                                                          Best Local Similarity 88.3
Matches 98; Conservative
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                                                                                                                   single
                                                                                                                                                            MOLECULE TYPE: peptide
                                                                                                                                        linear
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CLASSIFICATION:
                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94301
                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                 US-08-487-200-46
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TELEFAX:
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APPLICANT: Sladak, Anthony W.
APPLICANT: Bladak, Lisa K.
APPLICANT: Gilliland, Lisa K.
APPLICANT: Gordon, Marcia L.
APPLICANT: Bajorath, Jurgen
APPLICANT: Bajorath, Jurgen
APPLICANT: Bajorath, Jurgen
APPLICANT: Bajorath, Jurgen
TITLE OF INVENTION: Different Epitopes of Human gp39 and Methods For Their Use
TITLE OF INVENTION: In Diagnosis and Therapy
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DIVLTQSPASLAVSLGQRATISCRASKSVSASGYNYMHWYQQRAGQPPKLLIHLASNLES 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DIVUTQSPASLAVSLGQRATISCRASQSVSTSRYSYMHWYQQKPGQPAKLLIKFASNLES 60
                          1 DIVLTQSPASLAVSLGQRATISCRASKSVSASGYNYMHWYQQKAGQPPKLLIHLASNLES 60
                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Process for Generating Specific Antibodies NUMBER OF SEQUENCES: 61
NUMBER READABLE FORM:
MEDIUM TYPE: Ploppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 GVPARFSGSGSGTDFTLNIHPVEEEDASTYYCQHSGELPFTFGSGTKLEIK 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 GVPARFSGSGSGTDFTLNIHPVEEEDTATYYCQHSWEIPYTFGGGTKLEIK 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87.4%; Score 505; DB 5; Length 111;
86.5%; Pred. No. 2.4e-46;
Live 6; Mismatches 9; Indels
                                                                                        61 GVPARFSGSGSGTDFTLNIHPVEEEDASTYYCQHSGELPFTFGSGTKLEI 110
                                                                                                                   3: Bristol-Myers Squibb Company 3005 First Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/14106
                                                                                                                                                                                                                                                     Sequence 53, Application PC/TUS9414106 GENERAL INFORMATION: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5876950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 86.59
Matches 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US94-14106-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
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                                                                                                                                                                                                            RESULT 12
PCT-US94-14106-53
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APPLICANT: TOSI, CLAUDIO
APPLICANT: TOSI, CLAUDIO
APPLICANT: TOSI ANNA
TITLE OF INVENTION: RECOMBINANT VECTOR AND USE THEREOF FOR
TITLE OF INVENTION: EXCELLULAR PREPARATION OF SINGLE MOLECULA ANTIBODIES FROM
TITLE OF INVENTION: BACILLUS SUBTILIS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                    ó
                                                                                                                                                                                                                                                                                 1 DIVLTQSPASLAVSLGQRATISCRASKSVSASGYNYMHWYQQRAGQPPKLLIHLASNLES 60
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                                                                                                                                                                                                                                                                                                                                                                        61 GVPARFSGSGSGTDFTLNIHPVEEEDASTYYCQHSGELPFTFGSGTKLEIK 111
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89.1%; Pred. No. 1.2e-46;
tive 6; Mismatches 6; Indels
                                                                                                                                                                                      88.3%; Score 510; DB 4; Length 111; 88.3%; Pred. No. 7.2e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C. STREET: F.S. Jefferson Davis Highway, Suite 400 CITY: Arlington
                                                                                                                                                                                                                                    10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 08-MRR-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                    3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 08-MAR-1994
CLASSIFICATION: 435
ATTONNEY, FAGENT INFORMATION:
NAME: Oblon, No. 5674712man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 2264-061-0
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-220
TELEFAX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/08207169A Patent No. 5674712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 111 amino acids TYPE: amino acid
LENGTH: 111 amino acids
                                                                                                                                                                                                              Best_Local Similarity 88.39
Matches 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GRANDI, GUIDO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 87.9
Best Local Similarity 89.1
Matches 98; Conservative
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                        TYPE: amino acid
STRANDEDNESS: single
                                                                     TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-484-537-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-207-169A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                           Query Match
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                             E: Millen, White, Zelano & Branigan, P.C. 2200 Clarendon Boulevard, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95107967.2
FILLING DATE: 26-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Lebovitz, Richard M.
REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: MERCK 1781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/653,402B
FILING DATE: 24-MAY-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: June 28, 2001, 16:01:15
Job time: 523 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match

Best Local Similarity 87.4%;
Matches 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 146 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: protein US-08-653-402B-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                      CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                      U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                        22201
                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                         US-08-653-402B-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DIVLTQSPVSLAVSLGQRVTISCRASQSVSSSTNSYMHWYQQKPGQPPKLLIKYASNLES 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Process for Generating Specific Antibodies NUMBER OF SEQUENCES: 61
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 GVPARFSGSGSGTDFTLNIHPVEEEDASTYYCQHSGELPFTFGSGTKLEIK 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 GVPARFSGSGSGTDFTLNIHPVEEEDASTYYCQHSGELPFTFGSGTKLEIK 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86.5%; Score 500; DB 5; Length 218; larity 84.7%; Pred. No. 1.8e-45; Conservative 7; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86.9%; Score 502; DB 2;
86.5%; Pred. No. 6.2e-46;
tive 6; Mismatches 9
                               APPLICATION NUMBER: US/08/379,057
PILING DATE: 26-JAN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: POOT, Brian W.
REGISTRATION NUMBER: 32,928
REFERENCE/DOCKET NUMBER: ON0133-
TELEPHONE: (206) 727-3670
TELEPHONE: (206) 727-3670
TELEPHONE: (206) 727-3671
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 132 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US94/14106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 57, Application PC/TUS9414106 GENERAL INFORMATION: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
INFORMATION FOR SEQ ID NO: 57;
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
FRAGMENT TYPE: N-terminal
US-08-379-057-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 86.5%
Marches 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 218 amino acids
amino acid
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: protein PCT-US94-14106-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 94; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: ]
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PCT-US94-14106-57
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Sequence 12, Application US/08653402B
Fatent No. 5969107
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: CARCELLER, Ana
APPLICANT: GOMEZ, Alicia
APPLICANT: GOMEZ, Alicia
APPLICANT: PIULANS, Jaume
TITLE OF INVENTION: Anti-idiotypic antibodies which induce an
TITLE OF INVENTION: immune response against epidermal growth factor receptor.
CORRESPONDENCE: 13
CORRESPONDENCE: ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 489.5; DB 2; Length 146;
Pred. No. 1.5e-44;
5; Mismatches 8; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 GVPARFSGSGSGTDFTLNIHPVEEEDASTYYCQHSGELPFTFGSGTKLEIK 111
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein – protein search, using sw model

June 28, 2001, 15:58:45; Search time 234.85 Seconds (without alignments) 36.003 Million cell updates/sec Run on:

US-09-724-406-26

Perfect score: Title:

1 DIVLTQSPASLAVSLGQRAT.......CQHSGELPFTFGSGTKLEIK 111 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

219241 seqs, 76174552 residues Searched:

Total number of hits satisfying chosen parameters:

219241

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100% Listing first 45 summaries

PIR\_68:\* Database :

pir1:\* pir2:\* pir3:\* .....

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | Description   | Iq kappa chain V r | g kappa |        | Id kappa chain V r | onoclona | chain  | g kappa | q kappa | q light | q kappa chain | kappa  | . 0    | q kappa | g kappa | ь      | g kappa chain v | g kappa | g kappa | light  | g kappa | 6      | g kappa | q kappa | 53 specific sing | a kappa cha | kappa chain pr | q light chain | a light | g kappa |
|-----------|---------------|--------------------|---------|--------|--------------------|----------|--------|---------|---------|---------|---------------|--------|--------|---------|---------|--------|-----------------|---------|---------|--------|---------|--------|---------|---------|------------------|-------------|----------------|---------------|---------|---------|
| SUMMARIES | ID            | KVMS75             | KVMS84  | KVMS40 | A56169             | JC5810   | S45715 | S68241  | KVMS85  | S55027  | 808963        | KVMS43 | KVMS54 | KVMS08  | S24288  | PN0446 | KVMS83          | KVMS69  | S19972  | PH1077 | KVMSC1  | KVMS10 | S19976  | PH0092  | JC5322           | S19971      | PH1226         | PH1076        | S59640  | KVMS37  |
|           | DB            |                    | ~       | ٦      | 7                  | 7        | ~      | 7       |         | 7       | ~             | Н      | Н      | П       | ~       | ~      | -               | -       | 7       | 7      | Н       | -      | N       | ~       | ~                | 7           | 7              | ~             | 7       | 7       |
|           | Length        | 111                | 111     | 111    | 210                | 218      | 112    | 218     | 111     | 131     | 111           | 111    | 108    | 111     | 110     | 140    | 111             | 111     | 112     | 102    | 111     | 110    | 112     | 108     | 233              | 112         | 131            | 102           | 101     | 111     |
| d₽        | Query         | 92.7               | 2       | 91.3   | 0                  | 90.7     | 0      | ö       | 89.4    | 88.1    | 87.7          | 85.3   | 84.8   | 84.4    |         |        | 83.4            | 83.4    | 82.9    | 82.4   |         | 81.9   | 81.8    | 81.6    | 81.2             | •           |                | 90.6          | 79.8    | 79.4    |
|           | Score         | 536                | 534     | 528    | 524                | . 524    | 520    | 520     | 517     | 509     | 507           | 493    | 490    | 488     | 486.5   | 486    | 482             | 482     | 479     | 476    | ^       | 473.5  | 42      | 7.      | 469.5            | 468         | 468            | 466           | 461     | 459     |
|           | Result<br>No. | -                  | 7       | m      | 4                  | S        | 9      | 7       | 80      | 0       | 10            | 11     | 12     | 13      | 14      | 15     | 16              | 17      | 18      | 19     | 20      | 21     | 22      | 23      | 24               | 25          | 26             | 27            | 28      | 29      |

| Ig kappa chain V r<br>Ig kappa chain pre | Ig kappa chain V r<br>acetylcoline recep<br>Ig kappa chain V r<br>Ig kanna chain V r | ig kappa chain v r<br>Ig kappa chain v r<br>aberrant kappa tra<br>anti-dlycoprotein | Ig kappa chain V-J<br>Ig kappa chain V-J<br>Ig kappa chain V-J | Ig kappa chain v r<br>Ig kappa chain pre<br>Ig kappa chain V-J<br>Ig kappa chain V r |
|--|--|---|--|--|
| S63596<br>KVMSM6                         | PL0081<br>PC6027<br>KVMS80<br>KVMS50   | S52448<br>JL0073<br>D45722  | S09969<br>E53285<br>S09966                                     | S26343<br>KVMS32<br>S09965<br>PH0093   |
| 21.2                                     | 704-   | 000   | 777  | 0000   |
| 115                                      | 102  | 128<br>128<br>111   | 111  | 107<br>132<br>111<br>109   |
| 79.4                                     | 5.77   | 77.2  | 76.3<br>76.3<br>76.1   | 76.0<br>75.6<br>75.4<br>75.1   |
| 458<br>458                               | 448<br>446.5<br>446<br>446   | 446<br>446<br>444   | 441<br>441<br>440  | 439<br>437<br>436<br>434   |
| 30                                       | 3 3 3 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5  | 36<br>37<br>38  | 39<br>40<br>41   | 4 4 4 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5  |

## ALIGNMENTS

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| SULT | 3407 |
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Ig kappa chain V region (PC7175) - mouse (tentative sequence)
C;Species: Mus musculus (house mouse)
C;Sate: 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 31-Mar-2000
C;Accession: B01938; A01938
R;Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978

A;Title: Rearrangement of genetic information may produce immunoglobulin diversity. A;Reference number: A93204; MUID:79073152 A;Accession: B01938

A; Molecule type: protein
A; Residues: 1-11 <MELTC; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keyvords: heterotetramer; immunoglobulin
F; 6-94/Domain: immunoglobulin homology attMM>
F; 23-92/Disulfide bonds: #status predicted

0; Gaps Query Match 92.7%; Score 536; DB 1; Length 111; Best Local Similarity 91.9%; Pred. No. 1.6e-41; Matches 102; Conservative 5; Mismatches 4; Indels

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1 DIVLTQSPASLAVSLGQRATISCRASKSVSASGYNYMHWYQQKAGQPPKLLIHLASNLES 60 ò

1 DIVLIQSPASLAVSLGQRATISCRASKSVSTSGYSYMHWYQQKPGQPPKLLIYLASNLES 60 a

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### ~ KVMS84

Ig kappa chain V region (PC6684) - mouse (tentative sequence)
C;Species: Mus musculis (house mouse)
C;Species: Mus musculis (house mouse)
C;Date: 01-Sep-1981 #sequence\_revision 01-Sep-1981 #text\_change 31-Mar-2000
C;Accession: A01938
R;Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978

A;Title: Rearrangement of genetic information may produce immunoglobulin diversity. A;Reference number: A;3204; MUID:79073152 A;Accession: A01938

A. Molecule type: protein A. Residues: 1-111 <WEI> C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light ( hain disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into C:Superfamily: immunoglobulin V region; immunoglobulin homology C:Keywords: heterotetramer F:16-94/Domain: immunoglobulin homology <IMM>

RESULT KVMS40

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Chacession: 345715
R.Kim, H.H.; Kato, K.; Yamato, S.; Igarashi, T.; Matsunaga, C.; Ohtsuka, H.; Higuchl, R.Kim, H.H.; Kato, K.; Yamato, S.; Igarashi, T.; Matsunaga, C.; Ohtsuka, H.; Higuchl, R.F. Lett. 346, 246-250, 1994
A.Title: Application of (13)C NMR spectroscopy to paratope mapping for larger antigen A.Reference number: 345714; MUID: 94283606
A.Reference number: 345715
A.Recession: S45715
A.Recession: S45715
A.Residues: 1-112 < KIM>A.Molecule type: DNA
A.Residues: 1-112 < KIM>A.Residues: 1-114 < KIM>A.Residues: 1-114 < KIM>A.Residues: 1-115 < KIM>A.Residues: 1-115 < KIM>A.Residues: 1-116 < KIM>A.Residues: 1-117 < KIMA <
                                                                                                                                                                                                                                                                                                                                     monocional antibody 13-1 light chain - mouse
C;Species: Mus musculus (house mouse)
C;Species: Was musculus (house mouse)
C;Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000
C;Accession: JC5810
R;Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada, Blochem Biophys. Res. Commun. 240, 566-572, 1997
A;Title: Structural characterization of mouse monoclonal antibody 13-1 against a porp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Comment: This catalytic antibody has peroxidase oxidase. It is directed against a C;Superfamily: immunoglobulin V region; immunoglobulin homology F;16-94/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig kappa chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-Mar-1997 #sequence_revision 14-Nov-1997 #text_change 07-May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DIVLTQSPASLTVSLGQRATISCRASKSVSSSGXSYMHWYQQRPGQPPRVLIYLASNLES 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DIVLTQSPASLAVSLGQRATISCRASKSVSASGYNYMHWYQQKAGQPPKLLIHLASNLES 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DIVLTQSPASLAVSLGQRATISCRASKSVSASGYNYMHWYQQRAGQPPKLLIHLASNLES 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 GVPARFSGSGSGTDFTLNIHPVEEEDVATYYCQHSRELPLFFGAGTKLELK 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GVPARFSGSGSGTDFTLNIHPVEEEDASTYYCQHSGELPFTFGSGTKLEIK 111
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                                                                                                                                             Score 524; DB 2; Length 218;
Pred. No. 3.9e-40;
                                                                                                        61 GVPARFSGSGSGTDFTLNIHPVEEEDASTYYCQHSGELPFTFGSGTKLEIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90.0%; Score 520; DB 2; 88.3%; Pred. No. 4.5e-40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 90.7%;
Best Local Similarity 91.0%;
Matches 101; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: protein A; Residues: 1-218 <AKA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: JC5810
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Best Local S
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JC5810
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Jg kappa chain V region (clone 23.2) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Species: Mus musculus (house mouse)

C;Accession: A56169

R;Monfardini, C:, Kieber-Emmons, T:; VonFeldt, J.M.; O'Malley, B.; Rosenbaum, H.; Godill

A;Title: Recombinant antibodies in bloactive peptide design.

A;Reference number: A56169; MUID:95204454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: protein
A;Residues: 1-111 <MEI>
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (k
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into
C;Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ig kappa chain V region (PC7940) - mouse (tentative sequence)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Dacession: C01938; A01938
R;Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A;Fitle: Rearrangement of genetic information may produce immunoglobulin diversity.
A;Reference number: A93204; MUID:79073152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ó
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                                                                                                                                                                                                                                                                                                                                                                                                                            61 GVPARFSGSGSGTDFTLNIHPVEEEDASTYYCQHSGELPFTFGSGTKLEIK 111
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Pred. No. 3.8e-40;
7; Mismatches 5; Indels
                                                                                                        Length 111;
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A;Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-210 -MOND
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Indels
                                                                                                                                                                                 Indels
                                                                                                     Score 534; DB 1; I
Pred. No. 2.4e-41;
3; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 528; DB 1;
Pred. No. 8.4e-41;
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F;16-94/Domain: immunoglobulin homology <IMM>
F;23-92/Disulfide bonds: #status predicted
   F;23-92/Disulfide bonds: #status predicted
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                                                                                                            92.4%;
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92.8%;
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89.2%;
                                                                                                        Query Match
Best Local Similarity 92.8'
Matches 103; Conservative
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Best Local Similarity
Matches 103; Conserv
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1 DIVLTQSPASLAVSLGQRATISCRASKSVSASGYNYMHWYQQKAGQPPKLLIHLASNLES 60

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6; Indels

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If light chain precursor V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 23-Mus musculus (house mouse)
C;Date: 23-Mus musculus (house mouse)
C;Date: 23-Mus musculus (house mouse)
C;Date: 23-Musculus | 1955 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 | 1965 |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C.Species: Mus musculus (house mouse)
C.Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 21-Jan-2000
C.Accession: S09963
R.Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jaton, J.C.; Izui, S.
Eur. J. Immunol: 20, 771-777, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ig kappa chain V region (PC7043) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:L31404, NID:9476719; PIDN:AAA72437.1; PID:9476720
C;Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DIVLTQSPASIAVSLGQRATISCRASKSVSASGYNYMHWYQQKAGQPPKLLIHLASNLES 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 DIVLTQSPASLAVSLGQRATISCRASKSVSASGYNYMHWYQQKAGQPPKLLIHLASNLES 60
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61 GVPARFSGSGSGTDFTLNIQPVEEEDAAIYYCQHSRELPLTFGAGTKLELK 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 GVPARFSGSGSGTDFTLNIHPVEEEDASTYYCQHSGELPFTFGSGTKLEIK 111
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Pred. No. 5.1e-39;
8; Mismatches 6; Indels
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86.5%; Pred. No. 6.5e-39;
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F;36-114/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 88.19
Best Local Similarity 87.49
Matches 97; Conservative
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A; Residues: 1-131 <JEF>
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A; Residues: 1-111 <REI>
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                                                 Ig kappa chain V region (Mabl3-1) - mouse (fragment)

N'Alternate names: immunoglobulin light chain
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C;Accession: S68241; S68214
R;Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T. submitted to the EMBL Data Library, March 1994 formation of an antibody L-chain-porphyrian R; Reference number: S68241
                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-218 <TAK>
A; Residues: 1-218 <TAK>
A; Cross-references: EMBL: D29670; NID: 9473962; PIDN: BAA06141.1; PID: 9473963
R; Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.
FEBS Lett. 375, 273-276, 1995
A; Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin
A; Reference number: S68211; MUID: 96085223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Wolecule Lype: protein
A; Residues: 1-111 
A; Residues: 1-111 
A; Residues: 1-111 
A; Note: the PG1285 and PG4039 sequences are identical
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap and isulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Reywords: heterotetramer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Rearrangement of genetic information may produce immunoglobulin diversity. A;Reference number: A93204; MUID:79073152
A;Accession: A01939
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C;Date: 01-Sep.1981 #sequence_revision 01-Sep-1981 #text_change 31-Mar-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90.0%; Score 520; DB 2; Length 218; 89.2%; Pred. No. 9e-40; 1.ve 6; Mismatches 6; Indels
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89.2%; Pred. No. 8.2e-40;
Live 6; Mismatches 6; Indels
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
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R; Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
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A: Residues: 'NI', 3-212 <TAW>
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Best Local Similarity

Query Match

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A; Accession: S68214

A; Accession: S68241

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Query Match

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Local Similarity 84.7 nes 94; Conservative
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        C; Accession: A01940
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A; Residues: 1-111 <WED:
R; Mo. J. J. A.: Bona, C. A.; Holmdahl, R.
Bur. J. Immunol. 23, 2503-2510, 1993
A; Title: Variable region gene selection of immunoglobulin G-expressing B cells with spec
A; Reference number: $42176; MUID:94009207
A; Accession: $42187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Complex: M. immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin homology F:16-94/Domain: immunoglobulin homology F:16-94/Domain: immunoglobulin homology F:23-92/Disulfide bonds: #status predicted
C;Accession: A01937; S42187; S42190; S42189; S42188; S42191; S42192
R;Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A;Title: Rearrangement of genetic information may produce immunoglobulin diversity. A;Reference number: A93204; MUID:79073152
A;Accession: A01937
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C;Species: Mus musculus (house mouse)
C;Date: 01.Sep-1981 #sequence_revision 01-Sep-1981 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 10-99 <MOO>
A;Cross-references: EMBL:Z25454; NID:g407842; PIDN:CAA80941.1; PID:g407843
A;Note: V-kappa-21E; anti-collagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL;225446; NID:g407834; PIDN:CAA80933.1; PID:g407835
A;Note: V-kappa-21E; anti-collagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross_references: EMBL:225452; NID:g407840; PIDN:CAA80939.1; PID:g407841
A;Note: V-kappa-21E; anti-collagen
A;Accession: S42192
                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:225444; NID:9407832; PIDN:CAA80931.1; PID:9407833 A;Note: V-kappa-21E; anti-collagen A;Accession: S42194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;cross_references: EMBL:225458; NID:9407844; PIDN:CAA80945.1; PID:9407845
A;Note: V-kappa-21E; anti-collagen
A;Accession: S42190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 13-99 cMOF>
A;Cross-references: EMBL:225450; NID:9407838; PIDN:CAA80937.1; PID:9407839
A;Note: V-kappa-21E; anti-collagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:225448; NID:g407836; PIDN:CAA80935.1; PID:g407837
A;Note: V-kappa-21E; anti-collagen
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85.6%; Pred. No. 1.2e-37;
Live 7; Mismatches 9; Indels
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Matches 95; Conservative
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A; Residues: 10-99 <MOY>
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A; Residues: 10-99 <MOO>
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A; Residues: 10-99 <MOJ>
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A; Residues: 12-99 < MOW>
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A; Residues: 15-99 <MOA>
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by Apparation v. 1991 (1992)
C; Species: Mus musculus (house mouse)
C; Species: Was musculus (house mouse)
C; Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 21-Jan-2000
C; Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 21-Jan-2000
C; Ancession: C01937
A; Reference number: A93204; MUID: 79073152
A; Accession: C01937
A; Molecule type: protein
A; Residues: 1-11 (WEL)
A; Residues: 1-11 (WEL)
C; Complex: An immunoquolulin heterotetramer subunit consists of two identical light (hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C; Superfamily: immunoquolulin homology (immunoqlobulin homology C; Superfamily: immunoqlobulin homology (immunoqlobulin homology A/Monain: immunoqlobulin homology (immunoqlobulin homolo
                                                                                                                                                                                                                                                                                                                                         C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer
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A; Description: Cloning and sequencing of the cDNA coding for the variable regions of
A; Reference number: $24287
R;Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A;Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A;Reference number: A93204; MUID:79073152
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C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Jun-2000
C;Accession: S24288
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A;Accession: S24288
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-110 <MON>
A;Residues: 1-110 <MON>
A;Residues: BBL:X62703; NID:g51673; PIDN:CAA44576.1; PID:g1333958
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
F;16-94/Domain: immunoglobulin homology <IMM>
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1; Gaps 1; Query Match 84.2%; Score 486.5; DB 2; Length 110; Best Local Similarity 86.5%; Pred. No. 4.5e-37; Matches 96; Conservative 5; Mismatches 9; Indels 1 à 8

61 GVPARFSGSGSGTDFTLNIHPVEEEDASTYYCQHSGELPFTFGSGTKLEIK 111 õ

61 GVPARFSGSGSGTDFTLNIHPVEEDAATYYCQHIRE-PYTFGGGTKLEIK 110 유

RESULT 15

Ig kappa chain precursor V-II region - human (fragment) C;Species: Homo sapiens (man) C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000

C; Accession: PN0446

R.Kaluza, B.; Betzl, G.; Shao, H.; Diamantsein, T.; Weidle, U.H.

Gene 122, 321-328, 1992

Gene 122, 321-328, 1992

A.Title: A general method for chimerization of monoclonal antibodies by inverse polymera
A; Reference number: PN0446
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-140 < KAL>
A; Cross-references: GB:L02345
C; Superfamily: immunoglobulin V region; immunoglobulin homology
F; Pl-20/Domain: signal sequence #status predicted <SIG>F; 21-140/Product: Ig light chain kappa-2 V region #status predicted <MAT>
F; 36-114/Domain: immunoglobulin homology <IMM>

Gaps ;; Query Match 84.1%; Score 486; DB 2; Length 140; Best Local Similarity 87.4%; Pred. No. 6.4e-37; Matches 97; Conservative 4; Mismatches 8; Indels

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1 DIVLTQSPASLAVSLGQRATISCRASKSVSASGYNYMHWYQQKAGQPPKLLIHLASNLES 60 21 DIVLTQSPASLAVSLGQRATISYRASKSVSTSGYSYMHWNQQKPGQPPRLLIYLVSNLES 80 a ö

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

June 28, 2001, 15:54:38 ; Search time 105.36 Seconds (without alignments) 36.089 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-724-406-26 578 1 DIVLTQSPASLAVSLGQRAT.......CQHSGELPFTFGSGTKLEIK 111

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

93435 seqs, 34255486 residues Searched:

93435 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_39:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARTES

| script                     |            |            |            | mus        | mus        | -          | Snu        | mus        | P01669 mus musculu | P01664 mus musculu | mns        | P01662 mus musculu | P01660 mus musculu | P01661 mus musculu | mus        | P01656 mus musculu | P01654 mus musculu | P03977 mus musculu | P01655 mus musculu | Snm        | snw        | P01657 mus musculu | homo       | homo       | homo       | mus m      | P04431 homo sapien | 5 homo     | ношо       | рошо       | mus m      | P01680 mus musculu | P01594 homo sapien |
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| SUMMARIES                  | KV3S MOUSE | KV3R_MOUSE | KV3T_MOUSE | KV3U_MOUSE | KV3M_MOUSE | KV3V_MOUSE | KV30_MOUSE | KV3N_MOUSE | KV3Q_MOUSE         | KV3L_MOUSE         | KV3P_MOUSE | KV3J_MOUSE         | KV3H_MOUSE         | KV3I_MOUSE         | KV3K_MOUSE | KV3C_MOUSE         | KV3A_MOUSE         | KV3D_MOUSE         | KV3B_MOUSE         | KV3F_MOUSE | KV3G_MOUSE | KV3E_MOUSE         | KV4C_HUMAN | KV4A_HUMAN | KV4B_HUMAN | KV5P_MOUSE | KV1W_HUMAN         | KV3L_HUMAN | KV3M_HUMAN | KV3D_HUMAN | KV2G_MOUSE | KV4A_MOUSE         | KV1B_HUMAN         |
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|   |           |                     |  | Craniata; Vertebrata; B<br>Sciurognathi; Muridae;  | .03003;<br>Loh E., Schilling J., Hood L.E.;<br>information may produce immunoglobulin                        |   | FRAMEWORK 1.<br>COMPLEMENTARITY-DETERMINING<br>FRAMEWORK 2.<br>COMPLEMENTARITY-DETERMINING | FRAMEWORK 3.<br>COMPLEMENTARITY-DETERMINING<br>FRAMEWORK 4.<br>BY SIMILARITY. |  | KAGO<br>   | GSGT<br> :  <br>GAGT                                    |   |
|   |           | نہ                  | (e)  | Mu   | J.,  |   | Y-DE   | Y-DE  | F041E89AA7858523<br>core 536; DB 1;<br>ed. No. 8.5e-48;<br>Mismatches 4; | MY OC  | PFTF<br>  11<br>PLTF                                    | · •   |
|   | NTS       | 11<br>F             | date)<br>update)   | Ver  | Schilling J<br>ion may pro   |   | 1.<br>PARIT<br>2.<br>PARIT   | 3.<br>ARIT<br>4.<br>ITY.  | W; F041E89AA785<br>Score 536; DB<br>Pred. No. 8.5e<br>5; Mismatches      | NYMH<br>:      <br>SYMH  | SGEL<br>       <br>SREL                                 | .11 AA.<br>odate)<br>update)  |
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| 00000000000000000000000000000000000000  |           | 0,                  | (Re)   | mus muschlus (Mouse).<br>Eukaryota; Metazoa; Chordata;<br>Mammalia; Eutheria; Rodentia;<br>NCBI_TaxID=10090; | 3152<br>Gatm   | 85-7<br>KVN<br>18003  | 24<br>39<br>54   | 61<br>93<br>102<br>23<br>111  | CE 111 AA; 1201  ch 1 Similarity 91. 102; Conservative                   | DIVLTOSPASLAVSLGORATISCRASKSVSASCYNYMHWYQQKAGQPPKLLIHLASNLES<br> | GVPARFSGSGSGTDFTLNIHPVEEEDASTYYCQHSGELPFTFGSGTKLEIK<br> | SE STANDARI<br>986 (Rel. 01, 0<br>986 (Rel. 01, 1<br>999 (Rel. 38, 1<br>CHAIN V-III R |
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                                                      Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.; Rearrangement of genetic information may produce immunoglobulin
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                                                                                                                                                                                                                                                         COMPLEMENTARITY - DETERMINING 2.
                                                                                                                                                                                                                                                                                                                                                                           92.4%; Score 534; DB 1; Length 111; 92.8%; Pred. No. 1.4e-47; Live 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                   COMPLEMENTARITY - DETERMINING 3.
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                                                                                                                                                                                                                                                                                                                                      12039 MW; 1E46988341858526 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1G KAPPA CHAIN V-III REGION PC 7940.
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                                                                                          MEDLINE=79073152; PubMed=103003;
                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 92.8
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6:785-790(1978).
                                                                                                                                               Nature 276:785-790(1978).
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                                                                                                                                                            PIR; A01938; KVMS84.
InterPro; IPR003006; -.
Pfam; PF00047; 1g; 1.
Immunoglobulin V region.
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InterPro; IPR003006; -.
Pfam; PF00047; ig; 1.
Immunoglobulin V region.
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P01672;
                                                                                                                                     diversity."
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SEQUENCE
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DISULFID
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Best Local 9
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KV3T_MOUSE
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                                                                  Gaps
                                                   1 DIVLTQSPASLAVSLGQRATISCRASKSVSASGYNYMHWYQQKAGQPPKLLIHLASNLES 60
                                                                                                                                                                                                                                                                                                                                                                                                              Nature 276:785-790(1978).
-!- MISCELLANEOUS: THE PC 4285 AND PC 4039 SEQUENCES ARE IDENTICAL.
                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                        MEDELINE=79073152; PubMed=103003; Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.; "Rearrangement of genetic information may produce immunoglobulin
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                                                                                                        61 GVPARFSGSGSGTDFTLNIHPVEEEDASTYYCQHSGELPFTFGSGTKLEIK 111
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89.2%; Pred. No. 7.2e-46;
Live 6; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPLEMENTARITY - DETERMINING 1.
  Length 111;
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COMPLEMENTARITY-DETERMINING
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 Score 528; DB 1; Length 11
Pred. No. 5.5e-47;
2; Mismatches 6; Indels
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-III REGION PC 7043.
                                                                                                                                                                                                                            21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Lest annotation update)
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91.3%;
92.8%;
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               Similarity 92.8
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InterPro; IPR003006; -.
Pfam; PF00047; ig; 1.
Immunoglobulin V region.
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Best Local Similarity
Matches 99; Conserva
                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
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                            103;
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P01673;
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SEQUENCE
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    Query Match
               Best Local
Matches 10
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KV3M_MOUSE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                           Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
"Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Welgert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
"Rearrangement of genetic information may produce immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 GVPARFSGSGSGTDFTLNIHPVEEEDASTYYCQHSGELPFTFGSGTKLEIK 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRAMEWORK 1. COMPLEMENTARITY-DETERMINING 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85.3%; Score 493; DB 1; Length 11:
85.6%; Pred. No. 1.9e-43;
.ive 7; Mismatches 9; Indels
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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                                                                                                                    MEDLINE-79073152; PubMed-103003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-79073152; PubMed-103003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 276:785-790(1978).
PIR; A01940; KVMS54.
InterPro; IPR003006; -.
Pfam; PF00047; 19; 1.
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity 85.61
Matches 95; Conservative
                                                                                                                                                                                                               Nature 276:785-790(1978).
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                                                                                                                                                                                                                                                               InterPro; IPR003006; -. Pfam; PF00047; ig; 1.
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108
108 AA;
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                                                NCBI_TaxID=10090;
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P01674;
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                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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"Rearrangement of genetic information may produce immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84.4%; Score 488; DB 1; Length 111;
84.7%; Pred. No. 6.3e-43;
Live 8; Mismatches 9; Indels
            Length 108;
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    Score 490; DB 1; Length 10:
Pred. No. 3.8e-43;
5. Mismatches 10; Indels
                                                                                                                          61 GVPARFSGSGSGTDFTLNIHPVEEEDASTYYCQHSGELPFTFGSGTKL 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12071 MW; 7A4ADE4D6C256D29 CRC64;
                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-III REGION PC 6308.
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21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-III REGION PC 7183.
                                   5; Mismatches
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        84.8%;
86.1%;
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Best Local Similarity 84.7%;
Matches 94; Conservative
Query Match
Best Local Similar..ty 86.1%
                                                                                                                                                                                                        STANDARD;
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InterPro; IPR003006; -.
Pfam; PF00047; ig; 1.
Immunoglobulin V region.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                               Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.; Rearrangement of genetic information may produce immunoglobulin
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1G KAPPA CHAIN V-III REGION PC 7769.
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                                                                         MEDLINE=79073152; PubMed=103003;
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Matches 92; Conservative
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InterPro; IPR003006; -.
Pfam; PF00047; ig; 1.
Immunoglobulin V region.
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InterPro; IPR003006; -.
Pfam; PF00047; ig; 1.
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NCBI_TaxID=10090;
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P01669;
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DB 1; Length 111;

83.4%; Score 482;

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McKean D.J., Bell M., Potter M.;
"Mechanisms of antibody diversity: multiple genes encode structurally related mouse kappa variable regions.";
Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
-I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 03, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
1G KAPPA GHAIN V-III REGION PC 7210.
Mus musculus (Mouse).
Mus musculus (Mouse).
Musmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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COMPLEMENTARITY-DETERMINING
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83.8%; Pred. No. 2.5e-42;
iive 8; Mismatches 10; Indels
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21-JUL-1986 (Rel. 01, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
IG KAPPA CHAIN V-III REGION CBPC 101.
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 Best Local Similarity 83.8 Matches 93; Conservative
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InterPro; IPR003006; -.
Pfam; PF00047; ig; 1.
Immunoglobulin V region.
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Best Local Similarity
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P01664;
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P01668;
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KV3P_MOUSE
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MEDLINE-79012520; PubMed-99744;
MCKean D.J., Bell M., Potter M.;
McKhanisms of antibody diversity: multiple genes encode structurally related mouse kappa variable regions..;
Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                     Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
"Rearrangement of genetic information may produce immunoglobulin
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MEDLINE-79073152; PubMed-103003;
Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
"Rearrangement of genetic information may produce immunoglobulin
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                                                                                                                                                                                                                                                                                                          Length 110;
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COMPLEMENTARITY-DETERMINING 2.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-III REGION ABPC 22/PC 9245.
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                        MEDLINE-79073152; PubMed-103003;
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Best Local Similarity 82.98
                                                                                    PIR: D01937; KYMS10.
InterPro; IPR003006; -
Pfam; PF00047; ig; 1.
Immunoglobulin V region.
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MEDLINE=79012520; Pubmed=99744;

MECKEAN D.J., Bell M., Potter M.;

"Mechanisms of antibody diversity: multiple genes encode structurally related mouse kappa variable regions.";

Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).

-I. MISCELLANEOUS: THE PC 3741 AND TEPC 111 SEQUENCES ARE IDENTICAL. PIR: A01934; KVMS37.

Interpro: IPEN003006; ...

Interpro: PREN00306; ...

Inmunoglobulin V region.
                                                                                                             Gaps
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                                                                                                                                       1 DIVLTQSPASLAVSLGQRATISCRASKSVSASGYNYMHWYQQKAGQPPKLLIHLASNLES 60
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE (PC 3741).
MEDILLE-99073122; Pubmed-103003;
Wedgert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
"Rearrangement of genetic information may produce immunoglobulin
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                                                                               79.6%; Score 460; DB 1; Length 111; 80.2%; Pred. No. 4.3e-40; Live 10; Mismatches 12; Indels
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111 FRAMEWORR 4.
92 BY SIMILARITY.
111 D7DF0609303453CE CRC64;
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21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-III REGION PC 3741/TEPC 111.
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                                                                                                            89; Conservative
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MEDLINE-79012520; PubMed-99744;
McKean D.J., Bell M., Potter M.;
"Mechanisms of antibody diversity: multiple genes encode structurally
                                                                                                                                                                                                 Purstein Y., Schechter I.; Primary Structures of N-terminal extra peptide segments linked to "Primary structures of N-terminal extra peptide segments linked to precursors: implications on the organization and controlled expression of immunoglobulin genes.";
                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                      SEQUENCE OF 21-131.
MEDLINE=71140225; PubMed=4691517;
MEDLINE=7140225; PubMed=4691517;
McKean D.J., Potter M., Hood L.E.,
"Mouse immunoglobulin chains. Pattern of sequence variation among kappa chains with limited sequence differences.";
Biochemistry 12:760-771(1973).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IG KAPPA CHAIN V-III REGION MOPC 63.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    related mouse kappa variable regions.";
Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
PIR; A01935; KVMSMG.
InterPro: IPROMOG. -.
Pfam. PF00047; 1g; 1.
Immunoglobulin V region; Signal.
                                                     21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-III REGION MOPC 63 PRECURSOR.
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MEDLINE=78235887; PubMed=98179;
                                       21-JUL-1986 (Rel. 01, Created)
             STANDARD;
                                                                                                    Mus musculus (Mouse).
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YYJK\_MOUSE STANDARD; FP01663; ST-JUL-1986 (Rel. 01, Created)

RESULT 15
KV3K\_MOUSE
ID KV3K\_M
AC P01663
DT 21-JUL

Search completed: June 28, 2001, 15:54:39 Job time: 127 sec

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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-III REGION PC 4050.
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                                                                                                                  MEDLINE=79073152; PubMed=103003;
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Nature 276:785-790(1978)
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InterPro; IPR003006; -.
Pfam; PF00047; ig; 1.
Immunoglobulin V region.
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

June 28, 2001, 16:08:26 ; Search time 411.58 Seconds (without alignments) 35.682 Million cell updates/sec Run on:

US-09-724-406-26 578 1 DIVLTGSPASLAVSLGGRAT......CQHSGELPFTFGSGTKLEIK 111 Title: Perfect score:

Sequence:

425026 seqs, 132305027 residues Searched:

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Scoring table:

425026 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL\_16:\* Database :

sp\_archea:\*
sp\_bacteria:\*
sp\_fung1:\*
sp\_human:\*
sp\_nammal:\*
sp\_mammal:\* sp\_organelle:\* sp\_phage:\* sp\_plant:\* 10:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. sp\_unclassified:\*
sp\_vertebrate:\*
sp\_virus:\*

sp\_rodent:\*

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| Result |       | %<br>Query | %<br>Query |          |           |  |
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| 9      | 343.5 | 59.4       | 107        | 4        | 09UL81    | Obulg1 homo capton   |
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| 15     | 320.5 | 55.4       | 109        | ٠.       | Opril 85  | Course Francisch   |
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| Q91174 mus musculu<br>Q9u182 homo sapien<br>Q9nsd6 homo sapien<br>Q9np29 homo sapien<br>Q9et13 mus musculu<br>Q9h5z4 homo sapien | Q91502 sphoeroides Q91502 sphoeroides Q61243 mus musculu Q94656 homo sapien Q946775 homo sapien Q99604 homo sapien Q99604 homo sapien | Q91.005 sphoeroides<br>Q91.005 sphoeroides<br>Q97.041 meriones un<br>Q92.041 meriones un<br>Q95.040 rattus norv<br>Q91.05 mus musculu<br>Q91.02 mus musculu<br>Q91.02 mus q91.00 | Oguij6 homo sapien<br>Q93033 homo sapien<br>Q93033 homo sapien<br>Q9xsm6 saimiri sci<br>Q9yhil ginglymosto<br>Q46631 bos taurus |
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| Q9JL74<br>Q9UL82<br>Q9NSD6<br>Q9NP29<br>Q9ET13<br>Q9H5Z4   | Q91B02<br>Q61243<br>Q9UQ56<br>Q99603<br>Q99603<br>Q99604  | 291B05<br>Q9YHF8<br>Q9X041<br>Q9GSQ0<br>Q9JL85<br>Q9H0Z2   | 090176<br>093033<br>0938M6<br>097H11<br>046631  |
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## ALIGNMENTS

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-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                         fetus.";
Clin. Inmunol. Inmunopathol. 87:184-192(1998).
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
HOMO Saplens (Human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NCBL_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                  Myosin-reactive autoantibodies in rheumatic carditis and normal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 GVPARFSGSGSGTDFTLNIHPVEEEDASTYYCQHSGELPFTFGSGTKLEIK 111
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                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-98277139; PubMed-9614934;
WU X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109 AA; 11646 MW; 5F675C52EC7EE197 CRC64;
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                                                109 AA
                                                  PRT;
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MEDLINE=98277139; PubMed=9614934;
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InterPro; IPR003006; -.
InterPro; IPR003596; -.
Pfam; PF00047; 1g; 1.
SMART; SM00406; IGv; 1.
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                                                  PRELIMINARY;
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SEQUENCE
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 16, Last annotation update)
MYOSIN-FRACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEWBLrel. 13, Created)
01-MAY-2000 (TrEWBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
MYOSIN-REACTIVE IMMUNGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
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-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Gaps
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                                                                                                                                                                                                1 DIVLTQSPASLAVSLGQRATISCRASKSVSASGYNYMHWYQQKAGQPPKLLIHLASNLES 60
                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE-98277139; PubMed-9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
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                                                                                           61.8%; Score 357; DB 4; Length 108; 61.3%; Pred. No. 8.2e-32; Live 20; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;
108 AA; 11738 MW; C06681716C4D16F3 CRC64;
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HSSP, P01607; 1RRI
InterPro; IPR003006; -.
InterPro; IPR003596; -.
Pfam; PF00047; 1g, 1.
SMART; SM00406; IGV; 1.
                                                                                                                                                    68; Conservative
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                                                                                                                            Similarity
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67; Conservative
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CN 8.
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SEQUENCE
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Q9UL79
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                                                                                                                      Clin. Immunol. Immunopathol. 87:184-192(1998).
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
MYOSIN-REACTIVE IMMUNGCLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
HOMO sapiens (Human).
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-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
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                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                 Myosin-reactive autoantibodies in rheumatic carditis and normal
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BEDLINE-99277139; Pubmed-9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                       11501 MW; 070549FDE0754748 CRC64;
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                                                                MEDLINE-98277139; Pubmed-9614934;
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HSSP; P80362; 1WTL.
InterPro; IPR003006; --
InterPro; IPR003596; --
Pfam; PF00047; 19; 1.
SMART; SM00406; IGV; 1.
                                                                                                                                                        EMBL; AF035031; AAD56267.1;
                                                                                                                                                               HSSP; P01607; 1REI.
InterPro; IPR003006; -
InterPro; IPR003596; -
Pfam; PF00047; 1g; 1.
SMART; SMO0406; IGv; 1.
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                                                    SEQUENCE FROM N.A.
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NON_TER
SEQUENCE
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Q9UL81;
                                                                                                            fetus."
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59.4%; Score 343.5; DB 4; Length 107; 60.4%; Pred. No. 2.5e-30;

Query Match Best Local Similarity

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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
MYOSIN-REACTIVE IMMUNOSLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998).
-1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
      Gaps
                                    1 DIVLTQSPAS...AVSLGQRATISCRASKSVSASGYNYMHWYQQKAGQPPKLLIHLASNLES 60
                                                       4; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metaroa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                  61 GVPARFSGSGSGTDFTLNIHPVEEEDASTYYCQHSGELPFTFGSGTKLEIK 111
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Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 59.3%; Score 343; DB 4; Length 108; Best Local Similarity 60.4%; Pred. No. 2.8e-30; Matches 67; Conservative 16; Mismatches 24; Indels
  19; Indels
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Last annotation update)
                                                                                                                                                                                                                                                       108 AA
20; Mismatches
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SEQUENCE FROM N.A.
STRAIN=BALB/C; TISSUE=SPLEEN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAR-2001 (TrEMBLrel. 16,
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InterPro; IPR003596; -.
Pfam; PF00047; 1g; 1.
SMART; SM00406; IGV; 1.
NON TER 1.
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                                                                                                                       STRAIN-BALB/C; TISSUE-SPLEEN;
shinobara N., Demura T., Fukuda H.;
"Isolation of a novel type of vascular cell wall-specific monoclonal
antibody recognizing a cell polarity using a phage display subtraction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DIVLTQSPASLAVSLGQRATISCRASKSVSASGYNYMHWYQQKAGQPPKLLIHLASNLES 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.; "Construction and sequencing of the single-chain antibody gene of human TMF-alpha specific monoclonal antibody."; Ti 4 Chun i Ta Hsueh Pao 19:373-376(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
ANTI HUMAN TNF-ALPHA LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58.3%; Score 337; DB 11; Length 298; 56.8%; Pred. No. 4.3e-29; tive 20; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               229 GVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWTTPYTFGGGTKLEIK 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 GVPARFSGSGSGTDFTLNIHPVEEEDASTYYCQHSGELPFTFGSGTKLEIK 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.; Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AF262753; AAG23804.1; -. NON_TER 107 107
                                                                                                                                                                                                                                                                            Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AB036341; BAA88633.1; -.
HSSP, P01607; IREI.
InterPro; IPR003066; -.
InterPro; IPR003596; -.
InterPro; IPR0047; 49; 2.
SMART; SM00406; IGv; 1.
SEQUENCE 298 AA; 31867 MW; E0F96B8A17004317 CRC64;
Shinohara N., Demura T., Fukuda H.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON_TER 107 107
SEQUENCE 107 AA; 11784 MW; 2B15EEA6604A26C3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         107 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
"Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
antibody (Mab 7, its light and heavy chains) and construction of a
single chain antibody (scPt).";
submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, FRIS2311, AAD40242.1;
InterPro; IPR003006;
                                                                                                                                                                                                                                                                                                                                               01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAR-2001 (TrEMBLrel. 16, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DIVLTQSPASLAVSLGQRATISCRASKSVSASGYNYMHWYQQKAGQPPKLLIHLASNLES 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                             "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4; Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 GVPARFSGSGSGTDFTLNIHPVEEEDASTYYCQHSGELPFTFGSGTKLEIK 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M. Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57.2%; Score 330.5; DB 4; Length 59.5%; Pred. No. 6.8e-29; tive 18; Mismatches 24; Indels
                 61 VPDRFMGSGSGTDFTLIISSVQTEDLADXFCQQHYRTPFTFGSGTKL 107
62 VPARFSGSGSGTDFTLNIHPVEEEDASTYYCQHSGELPFTFGSGTKL 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            109 AA; 11928 MW; 243325F72C7DAC83 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAR-2001 (TrEMBLrel. 16, Last annotation update)
KAPPA LIGHT CHAIN OF WAB7 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               214 AA
                                                                                                                               01-WAY-2000 (TrEMBLrel. 13, Created) 01-WAY-2000 (TrEMBLrel. 13, Last sequol-MAR-2001 (TrEMBLrel. 16, Last annotation)
                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                    MEDLINE=98277139; PubMed=9614934;
                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN.
EMBL; AF035028; AAD56264.1; -
HSSP; P01789; 1MCP.
InterPro; IPR003006; -
InterPro; IPR003596; -
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                         PRELIMINARY;
                                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                       NCBI_TaxID=9606;
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SEQUENCE
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Best Local $
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Query Match
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"Characterization of cross-reactive monoclonal anti-myosin/anti-n-
acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF206024; ARF69122.1; -.,
Interpro; IPR003006; -.
Interpro; IPR003596; -.
Pfam; PF00047; ig; 1.
SWART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DIVLTQSPASLAVSLGQRATISCRASKSVSASGYNYMHWYQQKAGQPPKLLIHLASNLES 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 SLAVSLGQRATISCRASKS-VSASGYNYMHWYQQKAGQPPKLLIHLASNLESGVPARFSG 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 SLPVSLGDQASISCRSSQSLVHTNGNTYLHWYLQKPGQSPKLLIYKVSNRFSGVPDRFSG 61
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2001 (TrEMBLrel. 16, Last annotation update)
MONCCLONAL ANTI-IDIOTYPIC ANTIBODY NP30 IMMUNOGLOBULIN LIGHT CHAIN
VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-0CT-2000 (TrEMBLrel. 15, Created)
-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56.5%; Score 326.5; DB 11; Length 104; 63.1%; Pred. No. 1.8e-28; ttive 11; Mismatches 26; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 56.7%; Score 328; DB 11; Length 214; Best Local Similarity 56.8%; Pred. No. 2.8e-28; Matches 63; Conservative 18; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          104
11360 MW; 5DA8BBFD5F0AA1AE CRC64;
                                                                                                                                                                     214 214
214 AA: 23922 MW; 52BA205FDE995E2A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SGSGTDFTLNIHPVEEEDASTYYCQHSGELPFTFGSGTKLEIK 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       104 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                        PEGM: PF00047; 19; 2.
PROSITE: PS00290; IG_MHC; UNKNOWN_1.
SMART; SM00410; IG_11ke; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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Best Local Similarity 63.1%
Matches 65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
InterPro; iPR003600; -.
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104 AA;
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Q9U410
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SEQUENCE FROM N.A.

Song X.T., Feng Z.Q., Qiu Z.N., Li Y.Q., Huang H.L., Guan X.H.;

"Amplification, cloning and sequence analysis of the light chain
variable region gene of monoclonal anti-idiotypic antibody NP30 of
Schistosoma japonicum.";

Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
Schistosoma japonicum (Blood fluke).
Eukaryota; Metazoa; Platyhelminthes; Rhabditophora; Neodermata;
Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 VLTQSPASLAVSLGQRATISCRASKSVSASGYNYMHWYQQKAGQPPKLLIHLASNLESGV 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 LLTQSPAIMSASPGEKVTMTCSASSSVS----YVYWYLQKPGSSPRLLIYDTSNLASGV 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Sukaryota: Metazoa; Chordata; Czaniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5,
                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 56.5%; Score 326.5; DB 5; Length 106; 1 Similarity 58.7%; Pred. No. 1.8e-28; 64; Conservative 16; Mismatches 24; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 PARFSGSGSGTDFTLNIHPVEEEDASTYYCQHSGELPFTFGSGTKLEIK 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       114
: 12775 MW; 070E31E210D1CB01 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE 106 AA; 11478 MW; F20F544426BAE63E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clin. Immunol. Immunopathol. 87:184-192(1998).
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                                                                                                                                                                                                                        EMBL; AF207620; AAF19434.1; -. HSSP; P01679; ZFBJ.
InterPro; IPR0001308; -. InterPro; IPR0003066; -. InterPro; IPR003596; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF035034; AAD56270.1; -. InterPro; IPR003006; -. InterPro; IPR003596; -.
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SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                       Pfam; PF00047; ig; 1.
ProDom; PD000600; -; 1.
SMART; SM00406; IGV; 1.
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114 AA;
                                                               NCBI_TaxID=6182;
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56.4%; Score 326; DB 4; Length 114;

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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAR-2001 (TrEMBLrel. 16, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                          Gaps
                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                          2;
                                                                                                                                                                                                                                                                                                                                                                                                                      60 SGVPARFSGSGSGTDFTLNIHPVEEEDASTYXC-QHSGELPFTFGSGTKLEIK 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111
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Mu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
Best Local Similarity 59.3%; Pred. No. 2.2e-28;
Matches 67; Conservative 17; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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Search completed: June 28, 2001, 16:08:26 Job time: 954 sec

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Gaps

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Query Match 55.4%; Score 320.5; DB 4; Length 109; Best Local Similarity 57.1%; Pred. No. 8.5e-28; Matches 64; Conservative 23; Mismatches 20; Indels 5.

1 DIVLTQSPASLAVSLGQRATISCRASKSVSASGINYMHWYQQKAGQPPKLLIHLASNLES 60

> qq ò

61 GVPARFSGSGSGTDFTLNIHPVEEEDASTYYC-QHSGELPFTFGSGTKLEIK 111

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

June 28, 2001, 16:14:38; Search time 362.28 Seconds (without alignments) 2.510 Million cell updates/sec Run on:

US-09-724-406-28

1 RASKSVSASGYNYMH 15 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

412676 segs, 60623988 residues Searched:

412676 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

A\_Geneseq\_0601:\*

/SIDS8/gcgdata/geneseq/geneseqp/AA1980.DAT:\*
/SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:\*
/SIDS8/gcgdata/geneseq/geneseqp/AA1982.DAT:\*
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// SIDSS/gradata/genesseq/genesseqp/AA1995.DAT: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/SIDS8/gcgdata/geneseq/geneseqp/AA1998.DAT: /SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT: /SIDS8/gcgdata/geneseq/geneseqp/AA2000.DAT: /SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT

SUMMARIES

| Match Len<br>94.8<br>93.5<br>93.5<br>93.5<br>93.5<br>88.3 | DB 22 22 20 20 20 20 20 20 20 16 19 | 1D AAB3100 AAR3100 AAR39532 AAY39534 AAX39535 AAX39535 AAX39546 AAX39546 AAX79546 AAR74945 | Description Antibody variable Anti-carcinoembryo Murine COLI VK cha Humanised Murine C Humanised Murine C Humanised Murine C Humanised Murine C L-CORI Of anti-id Light chain of mon |
|---|-------------------------------------|--|--|
| ۳.  | 108 12                              | AAR13088   | Murine 184 light   |
| ٦.  | 110 16                              | AAR74956   | Imminoalobulin lia   |

| lobulin li<br>ht chain v<br>nal antibo<br>sequence | Protein sequence of Murine 340 Vl amin 31765 hybridoma VL N-terminal sequenc Licht chain variah | HNK-20 variable ka<br>Anti-idiotype anti<br>p12-k2. Synthetic<br>Anti-idiotype anti<br>Mouse anti-idiotype | antibod<br>HSP60-b<br>HSP60-b<br>VL regi     | Light Chain Variab<br>Murine FA79 antibo<br>Humanised F479 ant<br>GM-CSF receptor al<br>Humanised antibody<br>Murine 206 antibod<br>Human thyroid stim | of the liantipody antibody second from chain very human gp? antibody antibody antibody        |
|--|---|--|--|--|---|
| AAR74957<br>AAR90832<br>AAW22952<br>AAW86123       | AAW86119<br>AAY90821<br>AAR07456<br>AAR15442  | AAR95947<br>AAR74967<br>AAR28668<br>AAR74966<br>AAW19578   | AAR52659<br>AAB00998<br>AAB10019<br>AAR25721 | AAK60528<br>AAB69661<br>AAB69662<br>AAR85175<br>AAR85242<br>AAR85236   | AAW70938<br>AAR75483<br>AAW375483<br>AAR80272<br>AAR15440<br>AAW03723<br>AAR75457<br>AAR75459 |
| 16<br>17<br>18<br>20<br>20                         | 17 50 51 50 51 50 51 50 51 50 50 50 50 50 50 50 50 50 50 50 50 50                               | 17<br>16<br>13<br>18   | 21<br>21<br>21<br>13                         | 22<br>22<br>16<br>17<br>17   | 19<br>116<br>117<br>116<br>116  |
| 110  | 110   | 128<br>130<br>131<br>146<br>146  | 212 15 111 111 1111 1111                     | 111<br>22<br>111<br>111<br>111   | 17<br>15<br>132<br>1125<br>125<br>132<br>132<br>218   |
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| 88888  | 88888   | 88888<br>9999  | 68<br>64<br>61                               | 59<br>59<br>59<br>59   | 0000004444<br>000004444   |
| 113  | 119<br>119<br>100<br>100  | 22<br>23<br>24<br>25   | 25<br>25<br>30<br>30                         | 0 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8  | 88844444<br>000112844<br>1009   |

#### ALIGNMENTS

AAB35100 standard; Protein; 151 AA. 27-MAR-2001 (first entry) AAB35100; Н AAB35100 RESULT 

Antibody variable region fusion protein #4.

Filamentous phage; protein display; pVII; pIX; combinatorial antibody library.

Synthetic.

WO200071694-A1.

30-NOV-2000.

24-MAY-2000; 2000WO-US14433.

99US-0318786 25-MAY-1999;

(SCRI ) SCRIPPS RES INST

Gao C; Lerner RA, Janda KD, Wirsching P,

WPI; 2001-032030,04.

Novel filamentous phage encapsulating a genome encoding fusion polypeptide comprising exogenous polypeptide fused to amino terminus of pull and pIX proteins, for constructing diverse heterodimeric polypeptide array

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AAY39532 standard; protein; 110 AA.
                                                                         AAY39532
                                                                RESULT
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                  The present invention describes a filamentous phage encapsulating a genome encoding a fusion protein. This fusion protein comprises an experous protein fused to the amino terminus of a filamentous phage pVII or pix protein. This is useful in the design of proteins for medical, industrial, environmental and research applications.
                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       murine-human anti-carcinoembryonic antigen (CEA) chimeric antibody. Which can be used in in vitro immunoassays for the detection of CEA, and monitoring of tumour-associated antigen during therapy. It can also be used in vivo diagnostically, or in therapy for the treatment of tumours associated with colorectal and breast carcinomas, as well those of the gastrointestinal tract, lung, ovary and pancreas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anti-carcinoembryonic antigen chimeric antibodies - for diagnosis and therapy of carcinoma, e.g. breast or colorectal carcinoma
                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAQ71394 codes for AAR60564 the antibody light chain region of
                                                                                                                      Length 151;
                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                 Anti-carcinoembryonic antigen chimeric antibodies; CEAS; chimeric human-murine; breast or colorectal carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schlom J;
                                                                                                                                                                                                                                                                                                           Anti-carcinoembryonic antigen chimeric light chain Ab.
                                                                                                                     Score 73; DB 22;
Pred. No. 1.2e-05;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mezes PS, Rixon MW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (DOWC ) DOW CHEM CO.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
Example 1; Page 82-83; 90pp; English.
                                                                                                                                                                                                                                            AAR60564 standard; Protein; 110 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 11; Page 50; 67pp; English.
                                                                                                                      94.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        94WO-US01709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93US-0017570
                                                                                                                                                                                                                                                                                        25-APR-1995 (first entry)
                                                                                                                                            Conservative
                                                                                                                                                                  1 RASKSVSASGYNYMH 15
                                                                                                                                                                                       24 rasksvstsgynymh 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gourlie BB, Kaplan DA,
                                                                                                                                                                                                                                                                                                                                                                             Chimeric Mus muscaris.
                                                                                                                                                                                                                                                                                                                                                                                        Chimeric Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1994-294331/36.
                                                                                                                      Query Match
Best Local Similarity
Matches 14; Conserv
                                                                                       151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAQ71394
                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-FEB-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-FEB-1993;
                                                                                                                                                                                                                                                                                                                                                        light chain.
                                                                                                                                                                                                                                                                                                                                                                                                              WO9419466-A.
                                                                                        Seguence
                                                                                                                                                                                                                                                                  AAR60564;
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This sequence represents the murine COLI VK chain (COLIMUVK), and was used to obtain the humanised antibody (Ab) of the invention. The mumanised Ab, or its fragment, specifically binds to carcinoembryonic antigen (CEA). The Ab, optionally coupled to an effector or label, is used to treat or prevent CEA-expressing cancers (e.g. of breast, ovary, lung, stomach, or colon) and to detect CEA-expressing calls, either in vitro (optionally on a solid support) or in vivo (particularly by tumour imaging to identify tumours and metastases before surgery), for diagnosis or prognosis. It is not significantly immunogenic, i.e. the Ab does not induce a human anti-murine antibody or allergic response, or non-specific cytotoxicity, so can be administered repeatedly. It retains specificity for CEA, and has improved clearance (allowing efficient targeting) and
                                                                                                                                                           Antibody; human; carcinoembryonic antigen; CEA; cancer; tumour imaging; tumour identification; metastasis; diagnosis; mouse; VK chain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New antibody specific for treatment and diagnosis of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Harris WJ, Armour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carr FJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY39534 standard; protein; 110 AA.
                                                                                                       Murine COL1 VK chain (COL1MuVK).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; Fig 2; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                 98WO-US03680.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anderson WHK, Tempest PR,
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                                                   22-NOV-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 RASKSVSASGYNYMH 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            netabolic properties
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AAY39532;
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                                                                                                                                                                                                                                                  Mus sp
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AAY39534
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Gaps

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93.5%; Score 72; DB 15; Length 110; 93.3%; Pred. No. 1.2e-05; Live 1; Mismatches 0; Indels

Query Match 93.5 Best Local Similarity 93.3 Matches 14; Conservative

/note= "encoded by CAR"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents a humanised version of the murine COL1 VK chain, designated COL1REVK, and was used to obtain the humanised antibody (Ab) of the invention. The humanised Ab, or its fragment, specifically binds to carcinoembryonic antigen (CEA). The Ab, optionally coupled to an effector or label, is used to treat or prevent CEA-expressing cancers of breast, ovary, lung, stomach, or colon) and to detect CEA-expressing cells, either in vitro (optionally on a solid support) or in vivo (particularly by tumour imaging to identify tumours and metastases before surgery), for diagnosis or prognosis. It is not significantly immunogenic, i.e. the Ab does not induce a human anti-murine antibody or allergic response, or non-specific cytotoxicity, so can be administered repeatedly. It retains specificity for CEA, and has improved clearance (allowing efficient targeting) and metabolic
                                        Antibody; human; carcinoembryonic antigen; CEA; cancer; tumour imaging; tumour identification; metastasis; diagnosis; mouse; VK chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antibody; human; carcinoembryonic antigen; CEA; cancer; tumour imaging; tumour identification; metastasis; diagnosis; mouse; VK chain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New antibody specific for treatment and diagnosis of cancer
                                                                                                                                                                                                                                                                                                                                                                                                             Carr FJ, Harris WJ, Armour K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 110;
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Pred. No. 1.2e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
Humanised Murine COL1 VK chain (COL1REVK).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY39535 standard; protein; 110 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93.5%;
93.3%;
                                                                                                                                                                                                                                                                             98WO-US03680.
                                                                                                                                                                                                                                                                                                                      98WO-US03680
                                                                                                                                                                                                                                                                                                                                                                                                           Anderson WHK, Tempest PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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Best Local Similarity 93.3
Matches 14; Conservative
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                                                                                                                             Mus sp.
Homo sapiens.
                                                                                                                                                                                        WO9943817-A1
                                                                                                                                                                                                                                                                             25-FEB-1998;
                                                                                                                                                                                                                                                                                                                        25-FEB-1998;
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Homo sapiens
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                                                                                                       Synthetic.
                                      Antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
NAME OF THE PROPERTY OF THE PR
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This sequence represents a humanised version of the murine COL1 VK chain, designated COL1REVK, and was used to obtain the humanised antibody (Ab) of the invention. The humanised Ab, or its fragment, specifically binds to carcinoembryonic antigen (CEA). The Ab, optionally coupled to an effector or label, is used to treat or prevent CEA-expressing cancers (e.g. of breast, ovary, lung, stomach, or colon) and to detect CEA-expressing calls, either in vitro (optionally on a solid support) or in vivo (particularly by tumour imaging to identify tumours and metastases before surgery), for diagnosis or prognosis. It is not apinificantly immunogenic, i.e. the Ab does not induce a human anti-murine antibody or allergic responses, or non-specific cytotoxicity, so can be administered repeatedly. It retains specificity for CEA, and humanity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antibody; human; carcinoembryonic antigen; CEA; cancer; tumour imaging; tumour identification; metastasis; diagnosis; mouse; VK chain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New antibody specific for treatment and diagnosis of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                               Armour K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 72; DB 20; Length 11
Pred. No. 1.2e-05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Humanised Murine COL1 VK chain variant COL1VK HuVKF.
                                                                                                                                                                                                                                                                                                                                                                                                                         Anderson WHK, Tempest PR, Carr FJ, Harris WJ,
                       /note= "encoded by ATG"
                                                                               /note= "encoded by TGT"
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93.3%;
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Best Local Similarity 93.39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-550870/46.
                                                                                                                                                                                                                                                                                                                                                                 (DOWC ) DOW CHEM CO.
                                               Misc-difference 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    110 AA;
Misc-difference 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAZ20530
                                                                                                                                 W09943817-A1
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sequence is a humanised variant version of the murine COL1 VK chain,
                                                                                                                                                                                                                     designated COLINAVA.

The invention. The humanised Ab, or its fragment, specifically binds of the invention. The humanised Ab, or its fragment, specifically binds to carcinoembryonic antigen (CEA). The Ab, optionally coupled to an effector or label, is used to treat or prevent CEA-expressing cancers (e.g. of breast, ovary, lung, stomach, or colon) and to detect CEA-expressing calls, either in vitro (optionally on a solid support) or in vivo (particularly by tumour imaging to identify tumours and metastases before surgery), for diagnosis or prognosis. It is not significantly immunogenic, i.e. the Ab does not induce a human antibody or allergic response, or non-specific cytocoxicity, so can be administered repeatedly. It retains specificity for CEA, and has improved clearance (allowing efficient targeting) and metabolic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antibody; human; carcinoembryonic antigen; CEA; cancer; tumour imaging; tumour identification; metastasis; diagnosis; mouse; VK chain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 72; DB 20; Length 110;
pred. No. 1.2e-05;
1; Mismatches 0; Indels
                                                                                                                                                 New antibody specific for treatment and diagnosis of cancer
                                                                                       Harris WJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anderson WHK, Tempest PR, Carr FJ, Harris WJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Humanised Murine COL1 VK chain variant
                                                                                       Carr FJ,
                                                                                                                                                                               Disclosure; Page 44; 82pp; English.
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98WO-US03680
                             98WO-US03680
                                                                                       Anderson WHK, Tempest PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-NOV-1999 (first entry)
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                                                           (DOWC ) DOW CHEM CO.
                                                                                                                     WPI; 1999-550870/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 110 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                              properties.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antibody;
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                                     This sequence is a humanised variant version of the murine COL1 VK chain, designated COL1NWVK, and was used to obtain the humanised antibody (Ab) of the invention. The humanised Ab, or its fragment, specifically binds to carcinoembryonic antigen (CEA). The Ab, optionally coupled to an effector or label, is used to treat or prevent CEA-expressing cancers (e.g. of breast, ovary, lung, stomach, or colon) and to detect cancers in vivo (particularly by tumour imaging to identify tumours and metastases before surgery), for diagnosis or prognosis. It is not anti-murine antibody or allergic response, or non-specific cytotoxicity, so can be administered repeatedly. It retains specificity for CEA, and has improved clearance (allowing efficient targeting) and metabolic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A new anti-idiotype antibody against a human anticancer monoconal antibody is claimed. This antibody contains in its heavy chain 3 complemetarity determining regions CDR1 (AARR4929-RR4931), CDR2 (AARR4932-RR4935), this is also true of the light chain which has its own CDR1 (AARR4944-RR4946 and AAR85774), CDR2 (AARR4947-R74949) and CDR3 (AAR74950-R74954). The antibody and DNA encoding it are useful in pharmacological, medical and blochemical
                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            L-CDR-1 of anti-idiotype antibody against human anticancer antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel anti-idiotype antibody against an human anticancer monoclonal antibody - and DNA sequences encoding the antibody, useful in pharmacology, medicine and biochemical fields.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antibody; cancer; CDR; heavy chain; light chain; immunoglobulin; complementarity determining region.
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                                                                                                                                                                                                                                                                                                                                           Length 110;
                                                                                                                                                                                                                                                                                                                        Score 72; DB 20; Length LL. Pred. No. 1.2e-05;
                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
             Disclosure; Page 45; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR74945 standard; peptide; 16 AA.
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                                                                                                                                                                                                                                                                                                                                             93.5%;
93.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            1 RASKSVSASGYNYMH 15
                                                                                                                                                                                                                                                                                                                                                                                                                              24 rasksvsasgysymh 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1995-182987/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HAGI/) HAGIWARA Y.
                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                             Sequence 110 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JP07101999-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-OCT-1993;
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                                                                                                                                                                                                                                                                                                                                                                               14;
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                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
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16 AA;

Sequence

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The present sequence represents the light chain of monoclonal antibody
RS-2BB, which is directed against the respiratory syncytial virus (RSV).
The specification describes peptides which recognise, by
antigen-antibody type reactions, at least 1 epitope of a pathogenic virus
to CDR regions of monoclonal antibodies specific for RSV ARAV0917-2B are
analogous to CDR regions of monoclonal antibodies specific for site III
or IV of the VP6 protein of rota virus (RV). The peptides can neutralise
viral infections and may also inhibit fusion between infected and
uninfected cells or cells and viruses. They provide passive or active
protection and/or inhibit transcription of the virus, so are useful as
antiviral agents or for prophylaxis, in human or veterinary medicine. The
peptides can be labelled and used to diagnose infection or contamination
by the virus. The peptides are particularly directed against RSV or RS
contamination and any also be used against papilloma, adeno, entero, polio, influenza
                                        ö
                                      Gaps
                                                                                                                                                                                                                                                                                                                   Pathogenic virus; tropism; mucosa; CDR region; monoclonal antibody; respiratory syncytial virus; RSV; VP6 protein; rota virus; RV; viral infection; inhibit; fusion; protection; transcription; antiviral agent; prophylaxis; diagnosis; infection; contamination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New peptide(s) recognising viral epitope with tropism to mucosa useful for, e.g. diagnosing, preventing and treating viral infection(s)
                                      ö
Score 68; DB 16; Length 16;
Pred. No. 6.8e-06;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                       Light chain of monoclonal antibody RS-2B8.
                                                                                                                                                                                   AAW70952 standard; protein; 98 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pothier P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 2; 51pp; French.
 88.3%;
86.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or immune deficiency viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97FR-0000300.
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                                                                                                                                                                                                                                                      (first entry)
                                 Conservative
                                                                  1 RASKSVSASGYNYMH 15
                                                                                      Kohli E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYBO-) UNIV BOURGOGNE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-390320/34.
                 Local Similarity
hes 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bourgeois C,
                                                                                                                                                                                                                                                                                                                                                                                                                                          FR2758331-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-JAN-1997;
                                                                                                                                                                                                                                                    14-OCT-1998
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                                                                                                                                                                                                                    AAW70952;
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   Query Match
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                   Best Loc
Matches
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                                                                                                                                                 RESULT
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and murine CDRs (with the heavy chain framework mutated at sites near the CDRs), a human light chain framework and murine CDRs. It has a mean IC50 nearly equal to that of the murine monoclonal antibody from which the CDRs were derived. It is designated mutated Gal/Rel. The human Ig is capable of binding to a human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New recombinant immunoglobulin(s) reactive with leukocyte CD18 antigen - comprise human heavy chain framework and murine complementarity regions useful in treatment of inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A recombinant human Ig comprises a human heavy chain framework
                                                                                                                                                                                           Monoclonal antibody; complementarity determining region; CDR; integrin; hybridoma 184; protein REI; Gal/Rei; Ig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The murine CDRs are obtd. from murine hybridoma 1B4 (ATCC HB 10164). The light chain framework is derived from human myeloma protein REI (EP-239400). See also AAQ12682-84.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 68; DB 12;
Pred. No. 6.3e-05;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                    Singer II;
                                                                                                                                                               Murine 1B4 light chain-1 variable region.
                                                                                 AAR13088 standard; Protein; 108 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR74956 standard; Protein; 110 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                   Schmidt JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88.3%;
86.7%;
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                                                                                                                                  01-OCT-1991 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
38
                                                                                                                                                                                                                                                                                                                                                                        (MERI ) MERCK & CO INC.
                                                                                                                                                                                           Monoclonal antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RASKSVSASGYNYMH
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24 rasksvstsgysymh
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N-PSDB; AAQ12683.
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Matches 13: Conserv
                                                                                                                                                                                                                                                                                                                                                                                                   Mark GE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  108 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CD18 integrin.
                                                                                                                                                                                                                                                                                                   17-JAN-1991;
                                                                                                                                                                                                                               EP438312-A.
EP440351-A.
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                                                                                                          AAR13088;
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                                                      RESULT 10
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                                                                     AAR13088
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ID AAR7
XX
AC AAR7
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DT 19-J
XX
DE Immu
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Gaps

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Length 98;

Score 68; DB 19; Length 98 Pred. No. 5.6e-05; 1; Mismatches 1; Indels

Query Match 88.37
Best Local Similarity 86.77
Matches 13, Conservative

1 RASKSVSASGYNYMH 15

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WPI: 1995-182987/24.
                                                                                                                                                                         Sednence
                                                                                                                                                                                                                                                                                                                                                                                                       antibody.
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                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                        13
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                                                                                                                                                                                                                                                 AAR74955-R74959 are possible light chains of a new anti-idiotype antibody against a human anticancer monoconal antibody. This antibody contains in its heavy chain 3 complemetarity determining regions CDR1 (AAR74929-R74931), CDR2 (AAR74932-R794935) and CDR3 (AAR74936-R74936) this is also true of the light chain which has its own CDR1 (AAR74944-R74946 and AAR85774), CDR2 (AAR74947-R74946) and CDR3 (AAR74956-R74954). The antibody and DNA encoding it are useful in pharmacological, medical and biochemical fields.
                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                          Novel anti-idiotype antibody against an human anticancer monoclonal antibody - and DNA sequences encoding the antibody, useful in pharmacology, medicine and biochemical fields.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              \ensuremath{\operatorname{Immunoglobulin}} light chain of anti-idiotype antibody against human anticancer antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antibody; cancer; CDR; heavy chain; light chain; immunoglobulin; complementarity determining region.
                   Antibody; cancer; CDR; heavy chain; light chain; immunoglobulin;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR74957 standard; Protein; 110 AA.
                             complementarity determining region
                                                                                                                                                                                                                                  Claim 13; Page 4; 28pp; Japanese.
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Best Local Similarity 86.7:
Matches 13; Conservative
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24 rasksvstsgysymh 38
                                                                                                                                                              WPI; 1995-182987/24.
  anticancer antibody
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                                                                                                                                            (HAGI/) HAGIWARA Y.
                                                                                                                                                                        N-PSDB; AAQ90421.
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                                                                 JP07101999-A
                                                                                                       06-OCT-1993;
                                                                                                                          06-0CT-1993;
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                                                                                     18-APR-1995.
                                                                                                                                                                                                                                                                                                                                        Sednence
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                                               Mus sp.
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AAR90829-39 are monoclonal antibodies or a binding fragments produced by using insect guts, partic. insect brush border membranes (BBMs), esp. corn rootworm, as antigen; immunising a donor animal with the antigen; isolating immunocompetent B cells from the immunised animal; fusing B cells with a tumour cell line; isolating the fused cells, culturing them and cloning positive hybrid cells; and screening the hybrid cells for
                                                                                                                                                                                                                                                                   AAR74955-R74959 are possible light chains of a new anti-idiotype antibody against a human anticancer monoconal antibody. This antibody contains in its heavy chain 3 complemetarity determining regions CDR1 (AAR74929-R74931), CDR2 (AAR74932-R794935) and CDR3 (AAR74959-R74931), CDR2 (AAR74932-R794935) and CDR3 (AAR74954-R74946 and AAR857741, CDR2 (AAR74947-R74949) and CDR3 (AAR74950-R74954). The antibody and DNA encoding it are useful in pharmacological, medical and biochemical fields.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New monoclonal antibodies which bind insect gut proteins - used partic. with toxin moieties for the control of insect pests, partic. in plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 delta endotoxin; Bacillus thuringiensis; western corn rootworm; WCRW; maize; pesticide; brush border membrane vesicle; monoclonal;
                                                              Novel anti-idiotype antibody against an human anticancer monoclonal antibody - and DNA sequences encoding the antibody, useful in pharmacology, medicine and biochemical fields.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88.3%; Score 68; DB 16; Length 110;
86.7%; Pred. No. 6.4e-05;
.ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2B5 light chain variable region from pCIB4616.
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                                                                                                                                                                                                        Claim 14; Page 4; 28pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94US-0267641.
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N-PSDB; AAT15728.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            110 AA;
N-PSDB; AAQ90423
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prodn. of the required Mabs. The Mabs bind to the gut of a target insect but do not bind to mammalian BBMs. The DNA sequence can be operably linked to a toxin molety, esp. selected from e.g. Bacillus toxins, Pseudomonas exotoxin and phytolaccin, etc. The Abs are useful for control of insect pests, e.g. Coleoptera, Diptera, Hymenoptera and Lepidoptera. The pesticidal compsn. is pref. applied to a plant, e.g.
                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                          MAD 340; monoclonal antibody; foetal cell; pre-natal diagnosis; erythrocyte; trophoblast; genetic abnormality; foetal sex; analysis; epidermal growth factor receptor; EGFr; Down's syndrome; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Foetal cell analysis comprising isolating at least 2 sorts of foetal cell from maternal sample - specifically nucleated red cells and trophoblasts, useful for pre-natal diagnosis of genetic abnormalities or foetal sex
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Complementarity-determining region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Complementarity-determining region 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Complementarity-determining region 3"
                                                                                                                                         Score 68; DB 17; Length 110;
Pred. No. 6.4e-05;
!; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                    Monoclonal antibody (MAb) 340 light chain variable region.
                                                                                                                                                                  1; Indels
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/note= "Framework 4"
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/note= "Framework 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Framework 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                             AAW22952 standard; Protein; 110 AA.
                                                                                                                                       88.3%;
86.7%;
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                                                                                                                                                                 13; Conservative
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/note=
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101..11
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                                                                                                                                                     Best Local Similarity
                                                                                                     110 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAT75584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9730354-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Durrant LG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-AUG-1997
                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                     AAW22952;
                                                                                                                                         Query Match
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Example 2; Page 15; 31pp; English.

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This is the light chain variable region of a monoclonal antibody (MAb)
340. The MAb 340 acts as a trophoblast binding agent in a method for
analysing human foetal calls. The method comprises isolating at least 2
types of nucleated feetal calls. The method comprises isolating at least 2
types of nucleated feetal calls. The method comprises isolated bells
c specifically are nucleated red calls (erythrocytes) and trophoblasts.

CC The trophoblasts are isolated by contacting the maternal sample with a
c specific binding agent that binds to the epidermal growth factor receptor
(EGFr). MAb340 or an EGFr binding derivative of MAb340 comprising at
cc least the CDR regions of one or other of the light or heavy chain
carled regions of MAb 340 is used as the binding agent. Erythrocytes
cc are also isolated with a specific anti-transferrin antibody. The target
cc nucleotide sequences in the foetal cells are amplified by PCR primers.
The isolated cells can be used for genetic and biochemical analysis,
cparticularly to determine the sex of the foetus or to detect inherited
abnormalities, e.g. Down's syndrome. More generally MAb 340 can be used
cc carcinoma cells, that express EGF receptor. The method is not
carcinoma cells, that express EGF receptor. The method is not
carcinoma cells, that express EGF receptor. The method is not
carcinoma cells, that express EGF receptor. The method is not
concrete the types of cells significantly improves the sensitivity of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Non-immunogenic; epitope; T-cell; immunogenicity; immune system; SK; immunoglobulin; therapeutic; streptokinase; de-immunised.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Reducing immunogenicity of proteins - by modifying the amino acid sequence of the protein to eliminate potential epitopes for T-cells of a given species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88.3%; Score 68; DB 18; Length 110; 86.7%; Pred. No. 6.4e-05; 1ve 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein sequence of de-immunised 340 Vl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW86123 standard; Protein; 110 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Fig 5; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98GB-0007751.
97GB-0010480.
97GB-0016197.
97GB-0025270.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 86.7 nes 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RASKSVSASGTNYMH 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 rasksvstsgysymh
                                                                                                                                                                                                                                                                                                                                                                                pre-natal diagnosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                   110 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9852976-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-MAY-1998;
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02-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-MAY-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Matches
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proteins. The method comprises determining at least part of the amino acid sequence of the protein; (b) identifying in the amino acid sequence on or more potential epitopes for T-cells (T-cell epitopes) of the given species; and (c) modifying the amino acid sequence to eliminate at least one of the T-cell epitopes identified in step (b) thereby to eliminate or reduce the immunogenicity of the protein when exposed to the immunogenicity of the protein when exposed to the immunogenicity of the protein when exposed to the immuno to predict the basis for immunogenic responses is also provided. The methods can be used particularly for reducing the immunogenicity of immunoglobulins or therapeutic proteins, e.g. streptokinase (SK). The products can be used for diagnosis and therapy. The present sequence represents the protein sequence of de-immunised 340 Vh. invention relates to a method for the production of non-immunogenic 

110 AA; Sequence

; 0 0; Gaps 88.3%; Score 68; DB 20; Length 110; 86.7%; Pred. No. 6.4e-05; Live 1; Mismatches 1; Indels Query Match
Best Local Similarity 86.77
Matches 13; Conservative

1 RASKSVSASGYNYMH 15 ò

q

Search completed: June 28, 2001, 16:14:38 Job time: 1326 sec

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GenCore version 4.5

Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 28, 2001, 16:01:15; Search time 138.34 Seconds

(without alignments)

2.184 Million cell updates/sec

Perfect score: 77

Sequence: 1 RASKSVSASGYNYMH 15

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5
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Potal number of hits satisfying chosen parameters: 193259

193259 seqs, 20144635 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### Sequence 136, App Sequence 136, App Sequence 13, Appl Sequence 8, Appli Appli Appli Sequence 2, Appli Sequence 2, Appli Appl Appl App] 4pp] Sequence 1, Sequence 20, Sequence 8, Sequence 4, Sequence 46, Sequence 47 Sequence 2 Description Sequence 1 Sequence ( Sequence US-08-137-117D-136 US-08-436-717-136 US-08-318-970B-13 US-08-436-717-86 US-08-137-117D-25 US-08-436-717-25 US-08-653-402B-12 US-08-442-542-8 US-08-483-749A-20 -117D-86 PCT-US94-01709-2 US-08-712-212-1 PCT-US95-05160-1 US-08-765-469-8 US-08-137-117D-8 US-08-484-537-46 US-08-484-537-47 US-08-477-728-46 US-08-017-570-2 SUMMARIES Query Match Length DB Result . 9

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0; Gaps

93.5%; Score 72; DB 1; Length 110; 93.3%; Pred. No. 3.5e-05; ive 1; Mismatches 0; Indels

Query Match 93.5 Best Local Similarity 93.3 Matches 14; Conservative

1 RASKSVSASGYNYMH 15

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| App11            | Appl              | Appl             | Appl              | Appl             | Appl             | Appl             | Appl             | Appl             | Appl             | Appl              | Appl              | Appl             | Appl             | Appl             | Appl             | Appl              | Appl              |
|------------------|-------------------|------------------|-------------------|------------------|------------------|------------------|------------------|------------------|------------------|-------------------|-------------------|------------------|------------------|------------------|------------------|-------------------|-------------------|
| 6,               | 53,               | 16,              | 57,               | 30,              | 32,              | 11,              | 14.              | 30,              | 32,              | 30,               | 32                | 18               | 22,              | 18               | 22,              | 17                | 18,               |
| Sequence         | Seguence          | Sequence         | Sequence          | Sequence         | Sequence         | Sequence         | Seguence         | Sequence         | Sequence         | Sequence          | Sequence          | Sequence         | Seguence         | Sequence         | Sequence         | Sequence          | Sequence          |
| PCT-US95-15716-6 | PCT-US94-14106-53 | US-08-379-057-16 | PCT-US94-14106-57 | US-08-111-080-30 | US-08-111-080-32 | US-08-275-053-11 | US-08-275-053-14 | US-08-211-980-30 | US-08-211-980-32 | PCT-US93-07967-30 | PCT-US93-07967-32 | US-08-111-080-18 | US-08-111-080-22 | US-08-211-980-18 | US-08-211-980-22 | PCT-US92-07111-17 | PCT-US93-07967-18 |
| ស                | n                 | ~                | 'n                | П                | П                | -                | -                | 7                | Н                | 5                 | 5                 | Н                | -                | Н                | ~                | Ŋ                 | 5                 |
| 128              | 111               | 132              | 218               | 111              | 111              | 111              | 111              | 111              | 111              | 111               | 111               | 121              | 121              | 121              | 121              | 121               | 121               |
| 77.9             | 12.1              | 62.3             | 57.1              | 54.5             | 54.5             | 54.5             | 54.5             | 54.5             | 54.5             | 54.5              | 54.5              | 54.5             | 54.5             | 54.5             | 54.5             | 54.5              | 54.5              |
| 09               | o<br>o            | 48               | 44                | 42               | 42               | 42               | 42               | 42               | 42               | 42                | 42                | 42               | 42               | 42               | 42               | 42                | 42                |
| 28               | 67                | 30               | 31                | 32               | 33               | 34               | 35               | 36               | 37               | 38                | 39                | 40               | 41               | 42               | 43               | 44                | 45                |

#### ALIGNMENTS

```
RESULT 1

US-08-017-570-2

Sequence 2, Application US/08017570

Patent No. 5472693

GENERAL INFORMATION:

APPLICANT: GOTALE, BRIAN B

APPLICANT: RIXON, MARK W

APPLICANT: RAZAN, DONALD A

APPLICANT: RAZAN, DONALD A

APPLICANT: RAZAN, DONALD A

APPLICANT: MELSON

TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS: 24

CORRESPONDENCE ADDRESS: 24

CORRESPONDENCE ADDRESS: 32

CORRESPONDENCE ADDRESS: 32

COUNTRY: US

COUNTRY: US

COUNTRY: US

COMPUTER READABLE FORM:

MEDIAN TYPE: FLORPY disk

COMPUTER READABLE FORM:

MEDIAN TYPE: PLOPPY disk

COMPUTER READABLE FORM:

MEDIAN TYPE: PLOPPY disk

COMPUTER READABLE FORM:

MEDIAN TYPE: PLOPPY disk

COMPUTER READABLE FORM:

MEDIAN TYPE: ADDRESS: 34, 941

REPERENCE/DOCKET NUMBER: C.38, 777

TELECOMMUNICATION: UNDERFICE:

REGISTRATION INDRAMINION:

TELECOMMUNICATION OF 25

SEQUENCE CHARACTERISTICS:

LENGTH: 110 and mino acids

TOPOLOGY: linear

MOLECULE TYPE: PICOLE

US-08-017-570-2
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US-08-712-212-1
COUNTRY:
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APPLICANT: THE DOW CHEMICAL COMPANY
APPLICANT: U.S.A. DEPT. OF HEALTH AND HUMAN SERVICES
TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
CORRESPONDENCE ALDRESS:
ADDRESSE: Duane C. Ulmer
STREET: P.O. BOX 1967
CITY: Milland
                                                                                                                                                                           APPLICANT: RIXON, MARK W
APPLICANT: MEZES, PEFER S
APPLICANT: SCHLOM, DONALD A
APPLICANT: SCHLOM, JEFFREY
TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,426
FILING DATE: UG-JUN-1995
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 72; DB 1; 1
Pred. No. 3.5e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATE: 08-JUN-1995
FILING DATE: 16-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: ULMER, DUANE REGISTRATION NUMBER: 34,941
REFERENCE/DOCKET NUMBER: C-38,777
TELECHONE: (517) 636-8104
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 48641-1967
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application PC/TUS9401709 GENERAL INFORMATION:
                                                                                           Sequence 2, Application US/08471426 Patent No. 5808033 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: 110 amino acids
TOPOLOGY: 110.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93.5%;
                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Duane C. Ulmer STREET: P.O. Box 1967
                                                                                                                                                         APPLICANT: GOURLIE, BRIAN B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 93.3
Matches 14; Conservative
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  24 RASKSVSASGYSYMH 38
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                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-471-426-2
                                                           RESULT 2
US-08-471-426-2
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                                                                                                                                                                                                                                                                                                                                                                                              STATE:
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Gaps
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pred: No. 3.5e-05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Williams, William V.
APPLICANT: Kieber-Emmons, Thomas
APPLICANT: Weather, David B.
APPLICANT: Workeldt, Joan M.
APPLICANT: VonFeldt, Joan M.
TITLE OF INVENTION: Biologically active peptides and
TITLE OF INVENTION: methods of identifying the same
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION UNMBER:
FILING DATE: 03-08/712,212
FILING DATE: 03-8EP-1996
CLASSIFICATION 1435
PRIOR APPLICATION NUMBER: 08/08/712,212
ATOTON NUMBER: 08/235,404
FILING DATE: 29-APR-1994
ATOTON NUMBER: 39-APR-1994
ATOTON NUMBER: 33,229
REGISTRATION NUMBER: 33,229
REGISTRATION NUMBER: 33,229
REGISTRATION NUMBER: 31,229
REGISTRATION NUMBER: 31,229
RECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: No. 5837460ris
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
                                                                                                   OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                            APPLICATION NUMBER: PCT/US94/01709
                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: ULMER, DUANE C
REGISTRATION NUMBER: 34,941
REFERENCE/DOCKET NUMBER: 38,777-F
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08712212 Patent No. 5837460
ZIP: 48641-1967
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93.5%;
                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (517) 636-8104 INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                : 110 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 93.5
Best Local Similarity 93.3
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US94-01709-2
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                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION:
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TELEFAX: 215-568-3439

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                                                                                                                                                                                             89.6%; Score 69; DB 2; Length 20;
86.7%; Pred. No. 1.7e-05;
tive 2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application PC/TUS9505160
GENERAL INFORMATION:
APPLICANT: Williams, William V.
APPLICANT: Rieber-Emmons, Thomas
APPLICANT: Welner, David B.
APPLICANT: Worfeldt, Joan M.
TITLE OF INVENTION: Biologically active peptides and
TITLE OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: Norris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/235,404
FILING DATE: 29-APR-1994
CLASSIFICATION:
ATORNEY/AGENT INFORMATION:
NAME: Defluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: UDN-2245
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
: INFORMATION FOR SED ID NO: 1:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: One Liberty Place, 46th Floor CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WorldPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                             Query Match 89.6
Best Local Similarity 86.7
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 86.7
Matches 13; Conservative
                                                                    ; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-712-212-1
                                                                                                                                                                                                                                                                                                            2 RASKSVSSSGYSYMH 16
                                                                                                                                                                                                                                                                                 1 RASKSVSASGYNYMH 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
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PCT-US95-05160-1
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                                                                                      APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, KOh
APPLICANT: SATO, KOh
APPLICANT: BENDIG, Mary
APPLICANT: BONDES, Steven
APPLICANT: SALDANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
MINMER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONTENT AFFLICATION MURBER: US/08/137,117D
FILING DATE: 20-DEC-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY AGENT INFORMATION:
NAME: WEGNER, HAROAD C
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 25,258
REJERENCE/DOCKET NUMBER: 25,258
TELEFROMNUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFRAX: (202)672-5309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                      ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
                          Sequence 136, Application US/08137117D Patent No. 5795965
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-436-717-136
Sequence 136, Application US/08436717
Patent No. 5817790
GENERAL INFORMATICN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           136:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RASKSVSASGYNYMH 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: linear
US-08-137-117D-136
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Best Local Similarity
Matches 13; Conserv
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US-08-137-117D-136
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1 RASKSVSASGYNYMH 15

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RESULT
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hideaxi HAGIWARA, et al.
TITLE OF INVENTION: AMINO ACID SEQUENCES OF ANTI-IDIOTYPIC
TITLE OF INVENTION: ANTIBODIES AGAINST ANTI-CANCER HUMAN MONOCLONAL ANTIBODY
TITLE OF INVENTION: AND DNA BASE SEQUENCES ENCODING THOSE SEQUENCES
TITLE OF INVENTION: AND DNA BASE SEQUENCES ENCODING THOSE SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88.3%; Score 68; DB 2; Length 15; 86.7%; Pred. No. 1.9e-05; 1.9e-1; Mismatches 1; Indels
                                                     APPLICANT: SALDANHA, Jose
TITLE OF INVENTION: RESHARED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,717
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: W0 PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 53466/126/AAOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                         ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 13, Application US/08318970B Patent No. 5589573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: WEGNER, Harold C. REGISTRATION NUMBER: 25,258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 136:
SEQUENCE CHARACTERISTICS:
BENDIG, Mary
JONES, Steven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 88.3
Best Local Similarity 86.7
Matches 13; Conservative
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                                                                                                                                                     CORRESPONDENCE ADDRESS: ADDRESSE: Foley & L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 20007-5109
                                JONES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-318-970B-13
                                APPLICANT:
          APPLICANT:
                                                                                                                                                                                                                                                     STATE:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: Dell System 210; Intel 80 285 Microprocessor
OPERATING SYSTEM: MS DOS 3.3
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Pred. No. 2e-05;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:

APPLICANT: Carozzi, Nadine B.
APPLICANT: Carozzi, Michael G.
TITLE OF INVENTION: Antibodies which Bind to Insect Gut
TITLE OF INVENTION: Proteins and their Use
NUMBER OF SUCHENCES: 49
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC Compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 16-MAY-1995
CLASSIFICATION: 530
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OTHER INFORMATION: hypervariable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUDRESS:
CLASSEE: Classes:
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
COUNTRY: USA
                                                                                                                                                                        SOFTWARE: Word Perfect, Version 5.1 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318,970B FILING DATE: OCtober 6, 1994
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/267,641
FILLING DATE: 28-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 8, Application US/08442542 Patent No. 5686600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 32,943
                                                                                                                                                                                                                                                                                   ATTORNEY AGENT INFORMATION:
NAME: Richard A. Steinberg
REGISTRATION NUMBER: 26,588
REFERENCE/DOCKET NUMBER: 5.7
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                 TELEPRA: (703) 549-2282
TELEPRA: (703) 836-0106
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 88.3
Best Local Similarity 86.7
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 RASKSVSTSGYSYMH 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RASKSVSASGYNYMH 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
TOPOLOGY: linear
CITY: Alexandria
                     Virginia
: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10532
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                     STATE: V
COUNTRY:
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US-08-765-469-8
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Sequence 20, Application US/08483749A

Sequence 20, Application US/08483749A

GENERAL INFORMATION:

APPLICANT: RING, DAVID B.

TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS

NUMBER OF SEQUENCES: 33

CORRESPONDENCE ADDRESS:

ADDRESSE: CHIRON CORPORATION

STREET: INTELLECTUAL PROPERTY - R440, PO BOX 8097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 68; DB 3; Length 110;
Pred. No. 0.00016;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 68; DB 1; Length 110
Pred. No. 0.00016;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA

ZIP: 94662-8097

COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM:
PC-DOS/MS-DOS
SOFTWARE: PATENTIN RE-BASE #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,749A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
ATORNEY/AGENT INFORMATION:
NAMM: SAVEREIDE, PAUL B.
REGISTRATION NUMBER: 05.914
REFERENCE/DOCKET NUMBER: 05.914
REFIERENCE/DOCKET NUMBER: 05.914
REFERENCE/DOCKET NUMBER: 05.914
REFIERENCE/DOCKET NUMBER: 05.914
RELEPAX: (510) 655-354.2
INFORMATION FOR SED ID NO: 20: SEQUENCE CHARACTERISTICS:
LENGTH: 110 anino acids
TYPE: anino acids
TYPE: Anino acids
                      CGC 1750
REFERENCE/DOCKET NUMBER: CGC TELECOMMUNICATION INFORMATION: TELEPHONE: 919-541-8615 TELEFAX: 919-541-8619 INFORMATION FOR SEQ ID NO: 8 SEQUENCE CHARACTERISTICS: LENGTH: 110 amino acids TYPE: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88.3%;
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86.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 88.3
Best Local Similarity 86.7
Matches 13; Conservative
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Best Local Similarity 86.73
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: protein US-08-442-542-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) MOLECULE TYPE: protein US-08-483-749A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RASKSVSASGYNYMH 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24 RASKSVSTSGYSYMH 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMERYVILLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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RESULT 11

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Gaps
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0
Sequence 8, Application US/08765469

Patent No. 6069301

GENERAL INFORMATION:
APPLICANT: Carozzi, Nadine B.
APPLICANT: Carozzi, Nadine B.
APPLICANT: Koziel, Michael G.
TITLE OF INVENTION: Artibodies which Bind to Insect Gut
TITLE OF INVENTION: Proteins and their Use
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STRTE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 68; DB 3; Length 110;
Pred. No. 0.00016;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL 117D-86

Sequence 86, Application US/08137117D

Sequence 86, Application US/08137117D

Fatent No. 595965

GENERAL INFORMATION:
APPLICANT: SATO, Koh
APPLICANT: SATO, Koh
APPLICANT: SALDANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR

NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                         ZIP: 10532

ZIP: 10532

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURREWY APPLICATION DATA:
APPLICATION NUMBER: US/O8/755,469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Foley & Lardner
3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: GG 1750
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NIMBER: 08/267,641
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 919-541-8615
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 86.7
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: protein US-08-765-469-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 RASKSVSTSGYSYMH 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RASKSVSASGYNYMH 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 3000 K Št
CITY: Washington
STATE: D.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 20007-5109
                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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PRIOR APPLICATION DATA:
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Pred. No. 0.00019;
1; Mismatches 1; Indels
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Sequence 86, Application US/08436717

Patent No. 5817790

GENERAL INFORMATION:
APPLICANT: SATO(INA, Masayuki
APPLICANT: SATO(Koh
APPLICANT: BENDIG, MATY
APPLICANT: BENDIG, MATY
APPLICANT: BENDIG, MATY
APPLICANT: SALDANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
ADDRESSE: FOLEY & Lardner
STREET
            MEDIUM TYPE: FIOPPY disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/137,117D
FILING APPLICATION T30
PRIOR APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-95476
FILING DATE: 19-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, HALCH CA.
REGISTRATION NUMBER: 55,258
REFERENCE/DOCKET NUMBER: 55,258
REFERENCE/DOCKET NUMBER: 53466/126/AAOK
TELECOMMUNICATION INFORMATION:
THE FORMATION THE PROPARATION:
THE FORMATION THE PROPARATION:
THE POLICATION NUMBER: 53,258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMMUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88.3%;
86.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (202)672-5300
TELETEX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 86
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGIH: 130 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 88.3
Best Local Similarity 86.7
Matches 13, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 RASKSVSASGYNYMH 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43 RASKSVSTSGYSYMH 57
  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 20007-5109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Wash:
STATE: D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-137-117D-86
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US-08-436-717-86
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Score 68; DB 2; Length 130;
Pred. No. 0.00019;
1; Mismatches 1; Indels
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APPLICANT: TSICHIYA, Masayuki
APPLICANT: STOCH
APPLICANT: SENDIG, Mary
APPLICANT: JONES, Steven
APPLICANT: SLOANHA, JOSE
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117D
FILING DATE: 20-DEC-1993
CLASSIFICATION 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR.1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR.1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-32084
FILING DATE: J9-FEB.1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR.1991
ATORNEY/AGERT INFORMATION:
NAME: WEGNER HAROLD CC.
NAME: WEGNER HAROLD CC.
REFRENCE/DOCKET NUMBER: 53.466/126/AAOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 20007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
US-08-137-117D-25
; Sequence 25, Application US/08137117D
; Patent No. 5795965
                                                                                                                                                                                                                                                                                                                                                                                                                  86:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88.3%;
                                                                                                                                                                                                                                                                                                                                                                   TELEEAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 86
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 88.3
Best Local Similarity 86.7
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-436-717-86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 1:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RASKSVSASGYNYMH 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43 RASKSVSTSGYSYMH 57
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0
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Pred. No. 0.00019;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 25, Application US/08436717
Patent No. 5817790
GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: BENDIG, Mary
APPLICANT: JONES, Steven
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES:
CORRESPONDENCES:
ADDRESSE: FOLEY 6 Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Folgy & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,717
               FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, HAROID C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/126/AAOK
TELECOMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELERX: (202)672-5300
TELEX: 904136
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PULGATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 328476
FILING DATE: 25-APR-1991
ATTORNEY AGGINT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: WEGNER, Harold C. REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/126/AAOK
TELECOMMUNICATION INFORMATION:
APPLICATION NUMBER: JP 3-95476
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 86.7%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-137-117D-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RASKSVSASGYNYMH 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-436-717-25
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein – protein search, using sw model

Run on:

June 28, 2001, 15:58:46; Search time 234.85 Seconds (without alignments) 4.865 Million cell updates/sec

US-09-724-406-28 Perfect score:

1 RASKSVSASGYNYMH 15 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 seqs, 76174552 residues Searched:

219241 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100% Listing first 45 summaries

Database :

PIR\_68:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*

pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Description   | kappa chain<br>etylcoline re | Ig kappa chain V r<br>Ig kappa chain V r | kappa  | ig kappa chain V r<br>Iα kappa chain V r |        | 6      | berrant kappa | д карра | Ig Kappa chain V r | monocional antibod | ~      | q kappa | kappa  | light  | light chain |        | Iq light chain V r |        | Iq kappa chain V r | kappa  | kappa  | kappa  | kappa  | ti-qlyc | Ig kappa chain pre |
|---------------|------------------------------|--|--------|--|--------|--------|---------------|---------|--------------------|--------------------|--------|---------|--------|--------|-------------|--------|--------------------|--------|--------------------|--------|--------|--------|--------|---------|--------------------|
| ΩI            | A56169<br>PC6027             | PH0092<br>S24288                         | KVMS84 | KVMS85                                   | S45715 | S52448 | JL0073        | FN0446  | 306241<br>TFSP10   | JC5322             | KVMS40 | S09963  | KVMS54 | S55027 | PH1076      | PH1077 | S59640             | 863596 | PH0093             | S25462 | S26343 | S26344 | KVMS37 | D45722  | KVMSM6             |
| DB            | 000                          | 7 7                                      |        |  | 7      | ~      | ~             | ٦ ٢     | <b>4</b> C         | 4 (                | -      | ~       | 7      | 7      | ~           | ~      | 7                  | 7      | ~                  | 7      | 7      | 7      | -      | 7       | Н                  |
| Length        | 210                          | 110                                      | 111    | 111                                      | 112    | 128    | 128           | 7 0 10  | 218                | 233                | 111    | 111     | 108    | 131    | 102         | 102    | 101                | 115    | 109                | 91     | 107    | 107    | 111    | 111     | 131                |
| Query         | 0,00                         | 88.3                                     | 88.3   | 88.3                                     | 88.3   | 88.3   | 600           | 0.00    | 9 60               | 88.3               | 85.7   | 84.4    | Э.     | 9.92   |             | ö      | ω.                 | 67.5   | 'n.                |        | 54.5   | ٠      | 54.5   |         | . 54 . 5           |
| Score         | 688                          | 8 89                                     | 8 8    | 89                                       | 89     | 89     | 200           |         | 9 6                | 989                | 99     | 65      | 64     | 29     | 28          | 24     | 53                 | 52     | 43                 | 42     | 42     | 42     | 42     | 42      | 42                 |
| Result<br>No. | 170                          | u 4.                                     | in v   | , ,                                      | Φ.     | מי פ   | ונ            | 12      | 13                 | 14                 | 15     | 16      | 17     | 18     | 19          | 20     | 21                 | 22     | 23                 | 24     | 25     | 56     | 27     | 28      | 29                 |

| hypothetical prote | Id kappa chain V r | lectin-L6 - Atlant | hypothetical prote | hypothetical prote | xylanase (EC 3.2.1 | IP3 receptor, XIP3 | homeotic protein m | homeotic protein m | hypothetical prote | arginine decarboxy | genome polyprotein | Iq kappa chain V r | Id heavy chain V r | Ig light chain V r |
|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| T48446<br>E53285   | S19972             | A56941             | T01233             | B64164             | B53295             | A40743             | A39479             | 828390             | T20458             | B75544             | S51122             | PL0258             | 817608             | B49442             |
| 764 2              | 112 2              | 221 2              | 233 2              | 301 2              | 608 2              | 2693 2             | 320 1              | 321 1              | 346 2              | 662 2              | 112 2              | 94 2               | 96 2               | 96 2               |
| 54.5               | 53.2               | 53.2               | 53.2               | 53.2               | 53.2               | 53.2               | 51.9               | 51.9               | 51.9               | 51.9               | 9.05               | 50.0               | 49.4               | 49.4               |
| 42                 | 41                 | 41                 | 41                 | 41                 | 41                 | 41                 | 40                 | 40                 | 40                 | 40                 | 39                 | 38.5               | 38                 | 38                 |
| 30                 | 32                 | 33                 | 34                 | 35                 | 36                 | 37                 | 38                 | 39                 | 40                 | 41                 | 42                 | 43                 | 44                 | 45                 |

### ALIGNMENTS

Types chain V region (clone 23.2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: 19-oct-1995 #sequence\_revision 19-oct-1995 #text\_change 11-Jan-2000
C;Accession: A56169
R;Monfardini, C;Kieber-Emmons, T; VonFeldt, J.M.; O'Malley, B.; Rosenbaum, H.; God J. Biol. Chem. 270, 6628-6638, 1995
A;Title: Recombinant antibodies in bloactive peptide design.
A;Reference number: A56169; MUID:95204454
A;Reference number: A56169 MUID:95204454
A;Reference recomparies in the conceptual translation
A;Residues: 1-210 <MON>
A;Residues: 1-210 <MON>

C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin

Gaps <u>,</u> Length 210; Query Match 89.6%; Score 69; DB 2; Length 210 Best Local Similarity 86.7%; Pred. No. 0.00013; Matches 13; Conservative 2; Mismatches 0; Indels

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1 RASKSVSASGYNYMH 15 24 RASKSVSSSGTSYMH 38 ò

#### N RESULT

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acetylcoline receptor monoclonal antibody A7 light chain variable region - mouse (fra

C. Species: Mus musculus (house mouse)
C. Species: Mus musculus (house mouse)
C. Date: 31-Jan-1997 #sequence\_revision 31-Jan-1997 #text\_change 21-Jan-2000
C. Date: 31-Jan-1997 #sequence\_revision 31-Jan-1997 #text\_change 21-Jan-2000
C. Date: 31-Jan-1997 #sequence\_revision 31-Jan-1997 #text\_change 21-Jan-2000
R. Manory, F.: Yang, K.: Graus, Y.; de Baets, M.
Chinese J. Microbiol. Immunol. 16, 45-48, 1996
A; Title: Pathogenicity and sequence analysis of a mouse anti-AChR monoclonal antibody
A; Reference number: PC6026
A; Reference number: PC6026
A; Molecule type: mRNi
A; Molecule type: mRNi
A; Residues: 1-102 cMNNi
A; Residues: 1-102 cMNNi
A; Residues: 1-102 cMNNi
A; Cross-references: EMBL: X80961
C; Comment: This protein induces acetylcoline receptor loss and muscular weakness in m
C; Superfamily: immunoglobulin Noregion; immunoglobulin homology
F; 8-86/Domain: immunoglobulin homology < IMM>

Gaps ö 88.3%; Score 68; DB 2; Length 102; 86.7%; Pred. No. 9.1e-05; tive 1; Mismatches 1; Indels 13; Conservative Query Match Best Local Similar:ty

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1 RASKSVSASGYNYMH 15

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Score 68; DB 1; 1
Pred. No. 9.9e-05;
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Matches 13; Conservative
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Nature 276, 785-790, 1978
A; Molecule type: protein
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ses 13; Conserva
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C) Species: Mus muscullus (house mouse)

C) Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Jun-2000

C) Accession: $24288

R; Moncharmont, B.

R; Residues: $24287

R; Residues: $24288

R; Status: preliminary

R; Status: preliminary

R; Status: preliminary

R; Status: preliminary

R; Cores-treferences: EMBL: $62703; NID: 951673; PIDN: CAA44576.1; PID: 91333958

C; Supperfamily: Immunoglobulin V region; immunoglobulin

E; 16-94/Domain: immunoglobulin homology <IMM>
                                                                                                                  Ig Kappa chain V region (anti-cyclosporin F) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 21-Jan-2000
C;Accession: PH0092
R;Schmitter, D.; Poch, O.; Zeder, G.; Heinrich, G.F.; Kocher, H.P.; Quesniaux, V.F.J.; V. Jorg-1038, 1990
A;Title: Analysis of the structural diversity of monoclonal antibodies to cyclosporine. A;Reference number: PH0087; MUID:91042649
A;Accession: PH0092
A;Residues: 1-108 <SCH>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-94/Domain: immunoglobulin homology <IMM>F;24-94/Domain: immunoglobulin punctity-determining 1
F;54-60/Region: complementarity-determining 3
F;54-100/Region: complementarity-determining 3
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C; Species: Mus musculus (house mouse)
C; Accession: A01938
R; Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A; Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A; Reference number: A93204; MUID: 79073152
A; Accession: A01938
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86.7%; Pred. No. 9.8e-05
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86.7%;
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A; Residues: 1-111 <WEI>
A; Residues: 1-111 <WEI>
A; Note: the PC4285 and PC4039 sequences are identical
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer
Assidues: 1-111 (WEI)
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (
c;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (
hain disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer
F;16-94/Domain: immunoglobulin homology <IMM>
F;23-92/Disulfide bonds: #status predicted
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C;Species: Mus musculus (house mouse)
C;Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 31-Mar-2000
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Pred. No. 9.9e-05;
1; Mismatches 1;
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Pred. No. 9.9e-05;
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R;Kaluza, B.; Betzl, G.; Shao, H.; Diamantsein, T.; Weidle, U.H.
Gene 122, 321-328, 1992
A;Title: A general method for chimerization of monoclonal antibodies by inverse polym
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: S68241; S68214
R;Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, submitted to the EMBL Data Library, March 1994
A;Description: Specific peroxidase activity by formation of an antibody L-chain-porph A;Reference number: S58241
A;Accession: S68241
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A; Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyr A; Reference number: S68211; NUID:96085229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C.Species: Homo sapiens (man)
C.Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
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C; Species: Mus musculus (house mouse)
C; Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
                  C;Accession: JL0073
K;Carroll, W.L.; Mendel, E.; Levy, S.
MO! Immunol. 25, 991-995, 1988
A;Title: Hybridoma fusion cell lines contain an aberrant kappa transcript.
A;Reference number: JL0073; MUID:89112230
A;Accession: JL0073
A;Status: preliminary
A;Molecule type: mRNA
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A; Residues: 1-218 <TAK>
A; Cross-references: EMBL:D29670; NID:g473962; PIDN:BAA06141.1; PID:g473963
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
C;Reywords: signal sequence #status predicted <SIG>
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-140/Product: Ig light chain kappa-2 V region #status predicted <MAT>
F;36-114/Domain: immunoglobulin homology <IMM>
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;36-114/Domain: immunoglobulin homology <IMM>
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86.7%; Pred. No. 0.00011;
Live 1; Mismatches 1;
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86.7%; Pred. No. 0.00013;
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Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                    Ig Kappa chain V region - mouse (fragment)
Ig Kappa chain V region - mouse (fragment)
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 19-Mar-1997 #sequence_revision 14-Nov-1997 #text_change 07-May-1999
C; Accession: $4513
R; Kim, H.H.; Kato, K.; Yamato, S.; Igarashi, T.; Matsunaga, C.; Ohtsuka, H.; Higuchi, A. FBES Lett. 346, 246-256, 1994
R; Kim, H.H.; Kato, K.; Yamato, S.; Igarashi, T.; Matsunaga, C.; Ohtsuka, H.; Higuchi, A. FEBS Lett. 346, 246-256, 1994
R; Kim, H.H.; Kato, K.; Yamato, S.; Igarashi, T.; Matsunaga, C.; Ohtsuka, H.; Higuchi, A. Mille Sapination of (13)C NMR spectroscopy to paratope mapping for larger antigen-Fa A; Reference number: $45714; MuID:94283606
A; Reference number: $45715
A; Residues: 1-112 < KIM>A; Residues: 1-112 < KIMA
A; Residues: 1-112 < KIMA
A; Residues: 1-112 < K
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Submitted to the EMBL Data Library, November 1994
A;Description: Specific amplification by the polymerase chain reaction of rearranged gen
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C.Species: Mus musculus (house mouse)
C.Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C.Accession: 552448
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C:Species: Mus musculus (house mouse)
C:Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 21-Jan-2000
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Pred. No. 0.0001;
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Pred. No. 0.00011;
1; Mismatches 1; Indels
                  Indels
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                  1;
           1; Mismatches
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86.78;
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Matches 13; Conservative
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                                                                      1 RASKSVSASGYNYMH 15
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Matches 13; Conserv
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A:Molecule type: DNA
A:Residues: 1-128 <BER>
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Best Local Similarity 86.7
Matches 13; Conservative
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: JC5810
C;Accession: JC5810
C;Accession: JC5810
C;Accession: JC5810
C;Accession: JC5810
C;Accession: JC5810
A;Title: Structural characterization of mouse monoclonal antibody 13-1 against a porphyr A;Accession: JC5810
A;Accession: JC5
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A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 'NI',3-212 <TAM>
A;Cross-references: EMBL:D29670
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
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Best Local Similarity 86.7
Matches 13, Conservative
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Matches 14; Conservative
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C;Species: Mus musculus (house mouse)
C;Date: 30-Unn-1993 #sequence_revision 30-Jun-1993 #text_change 31-Mar-2000
C;Accession: C01938; A01938
R;Weigert, M.; Gatumitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A;Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A;Reference number: A93204; MUID:79073152
A;Accession: C01938
A;Accession: C01938
A;Accession: C01938
A;Residues: L-111 <WEID
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (C;Complex: An immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin monoglobulin homology
F;16-94/Nomain: immunoglobulin homology </td>
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Gaps ö

Length 111;

85.7%; Score 66; DB 1; Length 111 86.7%; Pred. No. 0.00022; Live 1; Mismatches 1; Indels

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

June 28, 2001, 15:54:39 ; Search time 105.36 Seconds (without alignments) 4.877 Million cell updates/sec Run on:

US-09-724-406-28

Title: Perfect score: Sequence:

1 RASKSVSASGYNYMH 15

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

93435 seqs, 34255486 residues Searched:

Total number of hits satisfying chosen parameters:

93435

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| NO.                             | Score<br>68<br>68<br>68<br>68                                | Match<br>88.3<br>88.3<br>88.3<br>88.3   | Length   | 88         | ID  KV3R_MOUSE  KV3R_MOUSE  KV3T_MOUSE  KV3T_MOUSE  | iption mus mus mus mus mus mus |
|---------------------------------|--|---|--|------------|---|--------------------------------|
| 11109876                        | 444444444444444444444444444444444444444                      |   | 108<br>131<br>131<br>221<br>608  |            | KV3H_MOUSE KV3H_MOUSE KV3X_MOUSE KV3X_MOUSE KV3X_MOUSE KV3I_MOUSE XV3Y_MOUSE XYXC_FIBSU XYNC_FIBSU                                | 40000404                       |
| 115<br>116<br>118<br>119<br>119 | 440<br>340<br>37.5<br>7.5                                    | 0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0. | 2468<br>2468<br>1111<br>132<br>334<br>816<br>821<br>265                    |            | MEC3_CAEEL MARB HUMAN KV3C_MOUSE KV3E_MOUSE ARCC_BUCAI NPAZ_MOUSE PZXS_HUMAN KNH1_CANGA   |                                |
| 32100987437                     | 36.5<br>36.5<br>36.5<br>36.5<br>36.3<br>35.3<br>35.3<br>35.3 | 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4   | 407<br>375<br>375<br>239<br>253<br>437<br>590<br>1651<br>121<br>121<br>123 | ннаннаннан | CHLP_SYNY3 PEL3_ERWCA PEL3_ERWCA KV3L_MOUSE US21_HOWVA YE24_MYCTU SGCC_ECOLI YM72_YEAST CO3_NAJNA RL20_CHLPN RL20_CHLPN WT2_INBLE |                                |

| P34764 caenorhabdi<br>Q42656 coffee arab<br>O84711 chlamydia t<br>P41582 citrobacter<br>P41583 citrobacter<br>P41575 klebsiella<br>P41575 klebsiella<br>P41578 shigella bo<br>P41579 shigella dy<br>P41580 shigella dy<br>P41580 shigella so<br>P77915 pseudomonas   |            | rata; Euteleostomi;<br>ridae: Murinae: Mus   | , Hood L.E.;<br>uce immunoglobulin | STERMINING 1. STERMINING 2. STERMINING 3.  | Length 111;<br>1; Indels 0; Gaps 0;  | ata; Euteleostomi;<br>idae; Murinae; Mus.   |
|--|------------|--|------------------------------------|--|--|---|
| 5 295 1 MEC3_CAEBR<br>5 378 1 AGAL_COFAR<br>4 45 1 GLPX_CHLTR<br>4 45 1 6PGD_CITPI<br>5 445 1 6PGD_CITPI<br>5 445 1 6PGD_ESCVU<br>6 445 1 6PGD_ESCVU<br>6 445 1 6PGD_SHIBO<br>6 445 1 6PGD_SHIBO<br>6 445 1 6PGD_SHISO<br>6 446 1 6PGD_SHISO | ALIGNMENTS | SIRNUARD;  1. 01, Created)  1. 01, Last sequence update)  1. 138, Last annotation update)  1. 186, Last annotation update)  1. 187, Constant Consta | 10300<br>Loh<br>info               | 13006; 19; 1.  V region.  Y region.  PRAMEWORK 1.  COMPLEMENTARITY-DETERMINING 38  COMPLEMENTARITY-DETERMINING 53  COMPLEMENTARITY-DETERMINING 92  RAMEWORK 3.  101  COMPLEMENTARITY-DETERMINING 111  FRAMEWORK 4. 92  BY SIMILARITY. 111  RA; 12039 MW; 1E46988341858526 CRC64; | 88.3%; Score 68; DB 1;<br>86.7%; Pred. No. 3e-05;<br>Live 1; Mismatches<br>15                      | JUDGE  KV35_MOUSE  KV35_MOUSE  FP01671;  21-JUD-1986 (Rel. 01, Created)  15-JUD-1986 (Rel. 01, Last sequence update)  15-JUD-1999 (Rel. 38, Last annotation update)  16 KAPPA CHAIN V-III REGION PC 7175.  Mus musculus; (Mouse).  Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; NCBI_TaxID=10090; |
| 34<br>35<br>36<br>37<br>37<br>37<br>37<br>37<br>44<br>42<br>42<br>37<br>45<br>45<br>45<br>45<br>45<br>45<br>45<br>45<br>45<br>45<br>45<br>45<br>45   |            | PO1670;<br>21-JUL-1986 (Re<br>21-JUL-1986 (Re<br>21-JUL-1999 (Re<br>15-JUL-1999 (Re<br>IG KAPPA CHAIN<br>Mus musculus (M<br>Eukaryota; Meta<br>Mammalia; Euther  |                                    | PIR; A01938; KV InterPro; IPROP P(am; PF000/1) Immunoglobulin DOMAIN 24 DOMAIN 24 DOMAIN 54 DOMAIN 54 DOMAIN 54 DOMAIN 54 DOMAIN 102 DISULFID 23 NON.TER 111   | Query Match Best Local Similarity Matches 13; Conservai Oy 1 RASKSVSASGYNYMH Db 24 RASKSVSTSGYSYMH | KV3S_MOUSE STAN TO FV15_MOUSE STAN AC P01671; DT 21-JUL-1986 (Rel. 0 DT 21-JUL-1999 (Rel. 3 DF 15-JUL-1999 (Rel. 3 DE IG KAPPA CHAIN V-II OS Mus musculus (Mouse OC Eukaryota; Metazoa; OC Mammalia; Eutheria; OX NCBI_TAXID=10090;   |

24 RASKSVSTSGYSYMH 38

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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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"Rearrangement of genetic information may produce immunoglobulin
                                                                  Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.; "Rearrangement of genetic information may produce immunoglobulin
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21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
1G KAPPA CHAIN V-III REGION PC 2485/PC 4039.
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Best Local Similarity 86.7
Matches 13; Conservative
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Nature 276:785-790(1978).
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InterPro; IPR003006; -.
Pfam; PF00047; ig; 1.
Immunoglobulin V region.
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Matches 13; Conserv
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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                                                                                                                                                                                Weigert M., Garmaiten L., Loh E., Schilling J., Hood L.E.;
"Rearrangement of genetic information may produce immunoglobulin
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Pred. No. 6.8e-05;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-III REGION PC 2154.
                                             21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG KARPA CHAIN V-III REGION PC 7940.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       85.7%;
86.7%;
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PIR, A01940; KVMS54.
InterPro; IPR003006; -.
Pfam; PF00047; 19; 1.
Immunoglobulin V region.
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Best Local Similarity 86.7
Matches 13; Conservative
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                        STANDARD;
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InterPro; IPR003006; -.
Pfam; PF00047; ig; 1.
Immunoglobulin V region.
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McKean D.J., Bell M., Potter M.;
McKennisms of antibody diversity: multiple genes encode structurally related mouse kappa variable regions.":
Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
-!- MISCELLANBOUS: THE PC 3741 AND TEPC 111 SEQUENCES ARE IDENTICAL.
PIR; A01934; KVMS37.
                                                                                                                                                  Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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 FRAMEWORK 2. COMPLEMENTARITY-DETERMINING 2.
                                    COMPLEMENTARITY - DETERMINING 3.
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COMPLEMENTARITY-DETERMINING 3.
                                                                                                                       Length 108;
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                                                                                                                    Score 64; DB 1; Length 108
Pred. No. 0.00015;
2; Mismatches 1; Indels
                                                                                  D40921D18DAC4B9E CRC64;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-III REGION PC 3741/TEPC 111.
                                                             BY SIMILARITY
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MEDLINE-79073152; PubMed-103003;
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80.0%;
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Best Local Similarity 53.3
Matches 8; Conservative
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24 RASESVDSYGNSFMH 38
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SECUENCE (ABPC 22).
MEDLINE=79012520; PubMed=99744;
MCKGan D.J., Bell M., Potter M.;
"Mechanisms of antibody diversity: multiple genes encode structurally related mouse kappa variable regions.";
Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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MEDLINE=79073152; PubMed=103003;
Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
"Rearrangement of genetic information may produce immunoglobulin
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NETURE 276:795-790(1978).
-!- MISCELLANEOUS: THE ABPC22 AND PC9241 SEQUENCES ARE IDENTICAL.
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"Rearrangement of genetic information may produce immunoglobulin
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                                                                21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-III REGION ABPC 22/PC 9245.
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21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
15 KAPPA CHAIN V-III REGION PC 4050.
111 AA
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InterPro; IPR003006; -.
Pfam; PF00047; ig; 1.
Immunoglobulin V region.
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InterPro; IPR003006; -.
Pfam; PF00047; ig; 1.
Immunoglobulin V region.
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"Mechanisms of antibody diversity: multiple genes encode structurally related mouse kappa variable regions.";
Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
PIR: A01935; KVMSM6.
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MCKean D.J., Potter M., Hood L.E.;
Mouse inmunoglobulin chains. Pattern of sequence variation among kappa chains with limited sequence differences.";
Biochemistry 12:760-771(1973).
                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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          COMPLEMENTARITY - DETERMINING 1.
                                   COMPLEMENTARITY - DETERMINING 2.
                                                           COMPLEMENTARITY - DETERMINING 3.
                                                                                                                                                 Score 42; DB 1; Length 111;
Pred. No. 1.2;
4; Mismatches 3; Indels
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                                                                                                              12005 MW; 39D87619313453CB CRC64;
                                                                                                                                                                                                                                                                                                                                               15-JUL-1999 (Rel. 38, Last annotation update) IG KAPPA CHAIN V-III REGION MOPC 63 PRECURSOR
                                                                                                                                                                                                                                                                                            131 AA.
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Pfam; PF00047; 1g; 1.
Immunoglobulin V region; Signal.
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MEDLINE=78235887; PubMed=98179;
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Best Local Similarity 53.3.
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131 AA;
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P01661;
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SEQUENCE
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"A novel type of limulus lectin-L6. Purification, primary structure, and antibacterial activity."
J. Biol. Chem. 270:14493-14499.
I- FUNCTION: LIPOPOLXSACCHARIDE-BINDING PROTEIN WITH GRAM-NEGATIVE ANTIBACTERIAL ACTIVITY. BINDS ZINC AND CALCIUM.
I- SUBCELLULAR LOCATION: L-GRANULES.
I- TISSUE SPECIFICITY: HEMOCYTES.
I- SIMILARITY: BELONGS TO THE TECTONIN FAMILY.
I- SIMILARITY: BELONGS TO THE TECTONIN FAMILY.
I- Lectin; Antibiotic; Zinc; Calcium; Metal-binding; Alkylation; Repeat.
DOMAIN
                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                         Tachypleus tridentatus (Japanese horseshoe crab).
Eukaryota, Metazoa, Arthropoda, Chelicerata, Merostomata, Xiphosura,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Haemophilus influenzae.
Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 221;
        DB 1; Length 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                              3; Indels
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                                                                                                                                                           30-WAY-2000 (Rel. 39, Created)
30-WAY-2000 (Rel. 39, Last sequence update)
30-WAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Score 42; UB . . No. 1.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.8;
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                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                  TISSUE=Hemocyte;
MEDLINE-95301536; PubMed=7782311;
                                4;
        54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53.2%;
72.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL PROTEIN HI1010. HI1010.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                Conservative
                                                                                                                                      STANDARD;
                                                      1 RASKSVSASGYNYMH 15
                                                                     44 RASESVDSYGNSFMH 58
                                                                                                                                                                                                                                   Limulidae; Tachypleus.
NCBI_TaxID=6853;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 KSVSASGYNYM 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        221 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
nes 8; Conserv
                   Best Local Similarity
Matches 8; Conserv
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[1]
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P44979;
                                                                                                                                      LEC6_TACTR
P82151;
                                                                                                                                                                                                 LECTIN L6.
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DISULFID
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        Query Match
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               STRAIN-RD / KW20 / ATCC 51907;
MEDLINE-95350630; PubMed=7542800;
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Rerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Soott J.D., Shilley R., Liu L. T., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gohm C.L., McDonald D.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL HYDROLASES).
                                                                                                                                                                                                                                            -1- SIMILARITY: BELONGS TO THE 3-HYDROXXISOBUTYRATE DEHYDROGENASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fibrobacter succinogenes (Bacteroides succinogenes).
Bacteria, Fibrobacter/Acidobacteria group, Fibrobacter group,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-1994 (Rel. 29, Last sequence update)
END-UL-1999 (Rel. 38, Last annotation update)
ENDO-1,4-BETA-XYLANASE C PRECURSOR (EC 3.2.1.8) (XYLANASE C)
(1,4-BETA-D-XYLAN XYLANOHYDROLASE C).
                                                                                                                                                                                               "Whole-genome random sequencing and assembly of Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53.2%; Score 41; DB 1; Length 301; 46.2%; Pred. No. 5.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7C615A25B0947D18 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               608 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00895; 3_HYDROXYISOBUT_DH; 1.
Hypothetical protein; Oxidoreductase; NAD.
ACT_SITE 177 177 BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND SEQUENCE OF 26-41.
                                                                                                                                                                                                                                                                  FAMILY. STRONG, TO E.COLI YGBJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AČT_SITE 177 177 B
SEQUENCE 301 AA; 31035 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-1994 (Rel. 29, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- PATHWAY: XYLAN DEGRADATION
                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U32782; AAC22671.1; -.
                                                                                                                                                                                                                              Science 269:496-512(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002204; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 SKSVSASGYNYMH 15
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49 AKAVAANGYDFAH 61
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                influenzae Rd."
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P35811;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fibrobacter
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Matches
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The mec-3 gene contains cis-acting elements mediating positive and negative regulation in cells produced by asymmetric cell division in Caenorhabditis elegans.";

Genes Dev. 5:2193-2211(1991).

-! FUNCTION: MEC-3 SPECIFIES DIFFERENTIATION OF THE SET OF SIX TOUCH RECEPTOR NUTGONES.

-STREET SIN THE MEC-3 GENE PROMOTER.

-- SUBCELLULAR COATION: NUCLEAR.

-- SUBCELLULAR COATION: NUCLEAR.

-- SUBCELLULAR COATION: NUCLEAR.
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=31233;
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                                                                                                                                                                                                                                                                                           InterPro; IPR001137; ...
Prompt Prompt Carlor Carlo
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NUCLEOPHILE (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTON DONOR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 41; DB 1; Length 608;
Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOPHILE (BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (LINKER).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     XYLANASE DOMAIN 2.
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01-FEB-1994 (Rel. 28, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               XYLANASE DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROTON DONOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE-92084094; PubMed-1684166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66415 MW;
                                                                                                                                                                                                                                              EMBL; U01037; AMA21848.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53.2%;
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Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MECHANOSENSORY PROTEIN 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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608
262
285
285
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543
142
237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              608 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Signal; Repeat
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ACT_SITE
SEQUENCE
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-1- FUNCTION: MEC-3 SPECIFIES DIFFERENTIATION OF THE SET OF SIX TOUCH
RECEPTOR NUCKON. BINDS COOPERATIVELY AS A HETERODIMER WITH UNC-86
TO SITES IN THE MEC-3 GENE PROMOTER.

-1- SUBCELLULAR LOCATION: NUCLEAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-88253425; PubMed-2898300;
Way J.C., Chaliie M.;
"mec-3, a homeobox-containing gene that specifies differentiation of the touch receptor neurons in C. elegans.";
Cell 54:5-16(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xue D., Finney M., Ruvkun G., Chalfie M.; Regulation of the mec-3 gene by the C.elegans homeoproteins UNC-86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- SIMILARITY: CONTAINS 2 LIM DOMAINS. THE LIM DOMAIN BINDS 2 ZINC
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                       PROSITE; PS00027; HOMEOBOX_1; FALSE_NEG.
PROSITE; PS50071; HOMEOBOX_2; 1.
PROSITE; PS00478; LIM_DOMAIN_1; 2.
PROSITE; PS00478; LIM_DOMAIN_1; 2.
HOMEOBOX; DNA-binding; Nuclear protein; Developmental protein;
Repeat; LIM motif; Metal-binding; Zinc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -! - SIMILARITY: TO OTHER HOMEOBOX DOMAINS. BELONGS TO THE LIM
                                                                                                                                                                                                                                                                                                                                                                                                               Score 40; DB 1; Length 320; Pred. No. 8.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Indels
                                                                                                                                                                                                                                                                                                                                                      ASP/GLU-RICH (ACIDIC).
AF98BD31C2B2FDB6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1988 (Rel. 09, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              321 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
                                                                                                                                                                                                                                                                                                                                         HOMEOBOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REVISIONS, SEQUENCE FROM N.A. MEDLINE-93099872; Pubmed-1361171;
                                                                                                                                                                                                                                                                                                                                                                     36849 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                    51.9%;
                                                                                 EMBL; X63956; CAA45377.1; -.
                                                                                                                                             InterPro; IPR001356; -.
InterPro; IPR001781; -.
Pfam; PF00412; LIM; 2.
Pfam; PF00046; homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 46.7
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MECHANOSENSORY PROTEIN 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 186 QVKKEVDAYGYNFEH 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RASKSVSASGYNYMH 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Caenorhabditis elegans
                                                                                                  PIR; A39479; A39479.
                                                                                                                                                                                                                                                                                                                                                      314
320 AA;
                                                                                                               HSSP; P06601; 1FJL.
TRANSFAC; T01970; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=6239;
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P09088;
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MEC3_CAEEL
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MEDINE-95104835; PubMed=7806212;
MEDINE-95104835; PubMed=7806212;
MEDINE-95104835; PubMed=7806212;
MEDINE-95104835; PubMed=7806212;
MIGHA Licent L., Feener C., Fischbach N., Kunkel L.M.;
Medining of human microtubule-associated protein 1B and the dentification of a related gene on chromosome 15.";
Genomics 22:273-280(1994).
Centric 32:273-280(1994).
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
MICROTUBULE-ASSOCIATED PROTEIN 1B [CONTAINS: MAP1 LIGHT CHAIN LCI].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00027; HOMEDBON_1: 1.
PROSITE; PS00478; LIM_DOMAIN_1: 2.
PROSITE; PS50023; LIM_DOMAIN_2: 2.
PROSITE; PS50071; HOMEDBON_2: 1.
HOMEOBON; DNA-binding; Nuclear protein; Developmental protein;
Repeat; LIM motif; Metal-binding; Zinc.
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51.9%; Score 40; DB 1; Length 321;
46.7%; Pred. No. 8.3;
Live 2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ASP/GLU-RICH (ACIDIC).
9231E7C3F5054853 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HOMEOBOX.
                                                                                                                                                                       EMBL; L02877; AAA50614.1; -.
EMBL; M20244; AAA28108.1; ALT_SEQ.
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315 321 A
321 AA; 37088 MW;
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                                                                                                                                                                                                                                                                                                         TRANSFAC: T01076; -.
InterPro: IPR001356; -.
Interpro: IPR001381; -.
Pfam: PF00412; LIM: 2.
Pfam: PF0046; homeobox: 1.
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Matches 7; Conservative
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                                                                                                                                                                                                                             PIR; A27662; A27662.
PIR; S28390; S28390.
HSSP; P06601; 1FJL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
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P46821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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-1- SIMILARITY: TO NEURAXIN.

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                                                                                                              A MIN: 15129; -.

R Interpro: IPR00102; -.

R Pfam: PF00414; MAPIB_neuraxin; 10.

DR PROSITE; PS00230; MAPIB_NEURAXIN; 6.

KW Microtubules; Repeat; Phosphorylation.

KW Microtubules: Repeat; Phosphorylation.

KW Microtubules: Repeat; Phosphorylation.

T 2468 MAPI LIGHT CHAIN LC1.

FT DOMAIN 589 T30 KKEE AND KKEI/V REPEATS.

12 X 17 AA TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                            270618 MW; 540839CBDF09D461 CRC64;
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SEQUENCE
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Search completed: June 28, 2001, 15:54:39 Job time: 127 sec

| :|| | |||:| 1911 RTTKSPSDSGYSY 1923

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1 RASKSVSASGYNY 13

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0; Gaps

3; Indels

51.9%; Score 40; DB 1; Length 2468; all arity 61.5%; Pred. No. 70; Conservative 2; Mismatches 3; Indels

Query Match Best Local Similarity Matches 8; Conserva

2; Mismatches

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

June 28, 2001, 16:08:26 ; Search time 411.58 Seconds (without alignments) 4.822 Million cell updates/sec Run on:

US-09-724-406-28 Title:

1 RASKSVSASGYNYMH 15 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

425026 seqs, 132305027 residues Searched:

425026 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

sp\_bacteria:\*
sp\_fung1:\*
sp\_human:\*
sp\_human:\*
sp\_invertebrate:\*
sp\_mamma1:\* sp\_unclassified:\*
sp\_vertebrate:\*
sp\_virus:\* sp\_organelle:\* sp\_rodent:\* SPTREMBL\_16:\* : sp\_archea:\* sp\_plant:\* sp\_phage: \* sp\_mhc:\* 9: 10:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No.     | Score<br>4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 | % Match Match 57.1 55.8 55.8 55.8 55.8 55.8 | Autch Length DB 57.1 477 10 55.8 240 2 554.5 764 110 | DB 70 70 70 70 70 70 70 70 70 70 70 70 70 | 1D<br>092WP7<br>091817<br>030925<br>091275 | Description Q9zwp7 pyrus pyrif Q91817 escherichia Q47197 escherichia 03025 escherichia |
|----------------|--|---|--|---|--|--|
| 0 / 80         | 444  | 53.55                                       | 203<br>232   | າທທ່                                      | P/85/0<br>Q9U5E9<br>Q9NKX8                 | P78570 agaricus bi<br>Q9u5e9 tachypleus<br>Q9nkx8 tachypleus                           |
| 9115           | 4 4 4  | 5.5.5.5                                     |  | 201                                       | 065278<br>Q9NB63<br>Q9FWU1                 | 065278 arabidopsis<br>Q9nb63 tachypleus<br>Q9fwul oryza sativ                          |
| 13             | 4 4 4<br>1 1 1 1                               | 53.2  | 2693<br>3469<br>3502                                 | 5 2                                       | 091908<br>Q9U412<br>Q9VYJ9                 | O91908 xenopus lae<br>O9u4i2 drosophila<br>O9vyj9 drosophila                           |
| 15             | 4 4<br>0 0                                     | 51.9  | 328<br>492   | សស  | 002240<br>076263                           | 002240 caenorhabdi<br>076263 drosophila  |
| 17<br>18<br>19 | 4 4 4<br>0 0 0                                 | 51.9<br>51.9<br>51.9                        | 662<br>1049<br>1095                                  | 0 to 10                                   | Q9RXR4<br>Q9VSV5<br>O9TVG7                 | Q9rxr4 deinococcus<br>Q9vsv5 drosophila<br>O9tva7 drosophila                           |

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01-OCT-2000 (TrEMBLrel. 15, Created) 01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)

90 AA.

PRT;

PRELIMINARY;

Q9L817 Q9L817;

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RESULT 2 Q9L817 ID Q9L817 AC Q9L817; DT 01-OCT DT 01-MAR

| Q9kjt6 staphylococ<br>Q82092 human rhino<br>Q9gyl0 mus musculu<br>Q59473 k 6-phospho<br>P70047 xenoous lae | 09vn58 drosophla<br>09ne91 leishmania<br>09m4y8 cucumis sat<br>09ky92 streptomyce | Q9kegs vibrio chol<br>Q9p734 neurospora<br>Q9wxel rhodovulum<br>Q98256 arabidopsis<br>Q9x69 orvetolagus | 048720 arabidopsis<br>Q9mlp0 arabidopsis<br>Q9s1h8 arabidopsis<br>Q9vr93 drosophila<br>Q9n1n7 drosophila | 03440; supplytocococococococococococococococococococ |
|--|---|---|--|--|
| Q9KJT6<br>Q82092<br>Q9QYL0<br>Q59473<br>P70047   | 09VN58<br>09NE91<br>09M4Y8<br>09KYG2  | Q9KSQ5<br>Q9P734<br>Q9WXE1<br>Q96256<br>Q9XT99  | 048720<br>Q9M1P0<br>Q9SJH8<br>Q9VF93<br>Q9NJN7   | 004086<br>004086<br>042025<br>037970<br>032402       |
| 2<br>11<br>13  | 5522  | 2<br>10<br>10   | 100 100 200 200 200 200 200 200 200 200  | 229622   |
| 257<br>112<br>170<br>445   | 1518<br>60<br>150<br>229  | 24 1 2 2 3 4 4 2 9 2 9 2  | 317<br>377<br>415<br>494   | 253<br>56<br>113<br>181<br>245<br>253                |
| 51.3<br>50.6<br>50.6<br>50.6   | 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4   | 4 4 4 4 4<br>2 0 0 0 0<br>4 4 4 4 4   | 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4  | 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4                |
|  | 5 8 8 8 8 6<br>6 6 6 6 6  |   | 33 33 33 34 34 34 34 34 34 34 34 34 34 3   | 37.5<br>37.5<br>33.7<br>33.7<br>33.7                 |
| 20<br>22<br>23<br>24<br>24   | 25<br>27<br>28<br>28<br>28  | 30<br>31<br>32<br>33  | # # # # # # # # # # # # # # # # # # #  | 0 4 4 4 4 4<br>0 0 11 2 2 2 4 4 5                    |

#### ALIGNMENTS

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MEDLINE-99138176; PubMed-9972231;
MEDLINE-99138176; PubMed-9972231;
Osaki H., Kudo A., Ohtsu Y.;
"Nucleotide sequence of seed- and pollen-transmitted double-stranded RNA, which encodes a putative RNA-dependent RNA polymerase, detected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                    01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-2099 (TrEMBLrel. 16, Last annotation update)
01-MAY-2001 (TrEMBLrel. 16, Last annotation update)
NANA-DEPENDENT RNA POLYMEASE.
Pyrus pyrifolia (Japanese pear) (Pyrus serotina).
Bukaryota: viridiplantee: Embryophyta: Tracheophyta: Spermatophyta:
Magnoliophyta: eudicotyledons; core eudicots: Rosaceae; Pyrus.
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                                                                                                                                                                                                                                                                                                                                                      from Japanese pear.";
Biosci. Biotechnol. Biochem. 62:2101-2106(1998).
EMBL. A001206: Bolymerase.
KNA-directed RNA. polymerase.
SEQUENCE 477 AA; 54908 MW; 071E9797E6B1C2F2 CRC64;
                                       477 AA
                                       PRT;
                                     PRELIMINARY;
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                                     Q9ZWP7
RESULT
                   Q9ZWP7
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Query Match
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                                                                                                                                                   Tanskanen J.M., Saarela S., Westerlund-Wikstroem B.A., Korhonen T.K.;
"The G-fimbrial chaperone protein.";
submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF21229; AAF72303 1;
InterPro; IPR001829;
Pfam; PF00455; pill_assembly; 1.
PRINTS; PR00969; CHAPERONFLII.
PROSITE; PS00635; PILI_CHAPERONE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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De Greve H.M.J., Heng P., Deboeck F., Yan H., Lintermans P.F.L.,
Hernalsteens J.P.;
Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
EMBL: L77091; AAA92619.1; -.
HSSP; P31697; 1BF8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                       Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                              55.8%; Score 43; DB 2; Length 90; 61.5%; Pred. No. 2;
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Promy: PR00345; pili_assembly; 1.
Prints; PR00969; CHAPERONFILI.
PRODOM; PD001447; -; 1.
PROSITE; PS00635; PILI_CHAPERONE; 1.
SEQUENCE 240 AA; 26469 MW; C82E5790CF5B9F35 CRC64;
                                                                                                                                                                                                                                                                                                                                                     90 AA; 10345 MW; 7E1EB1242E0946AA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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PUTATIVE G-FIMBRIAL CHAPERONE (FRAGMENT)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, 01-0CT-2000 (TrEMBLrel. 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel. 01,
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Best Local Similarity 61.5
Matches 8; Conservative
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Matches 8; Conservative
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                                    Escherichia coli
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                                                                                              NCBI_TaxID=562;
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01-NOV-1996
                                                                             Escherichia
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SEQUENCE
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030925
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Gaps
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Eukaryota, Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                              Lintermans P., Pohl P., Deboeck F., Bertels A.M., Schlicker C., Vandekerckhove J.S., Van Damme J., Van Montagu M.M., De Greve H.; "Isolation and nuclectide sequence of the F17-A gene encoding the structural protein of the F17 fimbriae in bovine enterotoxigenic Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bevan M., Terryn N., Ardiles W., Buysshaert C., Dasseville R., De Clerck R., De Keyser A., Neyt P., Rouze P., Van Den Daele H., Villarool R., Gielen J., Van Montagu M., Bancroft I., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                     Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-25KH09ST;
De Greve H., Heng P., Deboeck F., Lin H.Y., Schlicker C., Lintermans P., Hernalsteens J.-P.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, 87022140; AAA45720.1;
HSSP, P31097, 1BFB.
InterPro; IPR001829;
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL162875; CAB85556.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00345; pili_assembly; 1.
PRINTS; PR00969; CHAPERONPILI.
PRODOM; PD001447; -; 1.
PROSITE; PS00355; PILI_CHAPERONE; 1.
SEQUENCE 240 AA; 26455 MW; C83BB790CF5B9F35 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein.
SEQUENCE 764 AA; 86299 MW; AFEOE482FF091CB8 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
HYPOTHETICAL 86.3 KDA PROTEIN.
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Infect. Immun. 56:1475-1484(1988).
                                                                                                                                                                                                                                                                                                           MEDLINE-88226920; PubMed-2897333;
                                                                                                                                                                                                                                                 SEQUENCE OF 1-65 FROM N.A.
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Best Local Similarity 61.5%
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119 AGKSEKAQGYNYL 131
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                                                                                            Escherichia coli.
                                                                                                                                                                                  NCBI_TaxID=562;
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54.5%; Score 42; DB 10; Length 764;

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              Gaps
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Sonnenberg A.S.M., De Groot P.W.J., Schaap P.J., Baars J.J.P.,
Visser J., van Grienaven L.J.L.D.;
Tsolation of expressed sequence tags of Agaricus bisporus and their
assignment to chromosomes.";
Appl. Environ. Microbiol. 62:4542-4547(1996).
-I. CATALYTIC ACTIVITY: NUCLEOSIDE TRIPHOSPHATE = N PYROPHOSPHATE +
RNA(N) (BX SIMILARITY).
-I. SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA CHAIN FAMILY.
InterPro. IPR001572;
-InterPro. IPR001572;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tachypleus tridentatus (Japanese horseshoe crab).
Bukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
Limulidae; Tachypleus.
NCBI_TaxID=6853;
                                                                                                                            01-MAY-1997 (Tremblrel. 03, Created)
01-MAY-1997 (Tremblrel. 03, Last sequence update)
01-MAR-2001 (Tremblrel. 16, Last annotation update)
DNA-DIRECTED RNA POLYWERASE I (EC 2.7.7.6) (RNA POLYMERASE II) (RNA POLYMERASE III) (RNA NUCLEOTIDYLTRANSFERASE (DNA-DIRECTED))
                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00562; RNA_pol_B; 1.
DNA-directed RNA polymerase; Nucleotidyltransferase; Transcription;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-20076430; Pubmed-10608824;
MRGJai T., Kawabata, Si, Shishikura F., Sugita H.;
"Purification, characterization, and amino acid sequence of an embryonic lectin in perivitelline fluid of the horseshoe crab.";
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                                                                                                                                                                                              Agaricus bisporus (Common mushroom).
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Agaricales;
Agaricaceae; Agaricus.
NCBI_TaxID=5341;
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             Indels
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Last annotation update)
             5.
                                                                                                            114 AA
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            Mismatches
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   Pred. No.
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50.08;
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            7; Conservative
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                                                                                                          PRELIMINARY;
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                               2 ASKSVSASGYNYMH 15
                                           : |:|:||:|: |
13 SQKNVAASGHNHHH 26
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114 AA;
Best Local Similarity
Matches 7; Conserv
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Best Local Similarity
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SEQUENCE
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Q9U5E9;
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P78570
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Limulidae; Tachypleus.
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F6N23.7 OR AT4G00690.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                              Length 203;
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"Tachylectin-lemb.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB037394; BAA90326.1; -
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                                                                                    30900733AC2C89D2 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
TACHYLECTIN-1 EMBRYO (FRAGMENT).
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Last annotation update)
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13;
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2
                                                                                                                                            Score 41; DB 5
Pred. No. 11;
1; Mismatches
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Pred. No.
J. Biol. Chem. 274:37673-37678(1999).
EMBL; AB028144; BAA88574.1; -.
NON_TER 1 1
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01-AGG-1998 (TrEMBLrel. 07, Last seq
01-MAR-2001 (TrEMBLrel. 16, Last seno
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                                                                                  203 AA; 22550 MW;
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72.78;
                                                                                                                                         Query Match 53.2%;
Best Local Similarity 72.7%;
Matches 8; Conservative
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Best Local Similarity 72.7
Matches 8; Conservative
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                                                                                                                                                                                                                          4 KSVSASGYNYM 14
                                                                                                                                                                                                                                              85 KHVSASGYGYI 95
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                                                               NON_TER
SEQUENCE
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Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae;
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                                                                                    SEQUENCE FROM N.A.
                                            NCBI_TaxID=4530;
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SEQUENCE 2690
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Q9U4I2;
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Q9U4I2
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Q91908
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Chen S.-C., Yeh M.-S., Chiou S.-T., Huang C.-J., Liu T.-Y.;
Chen S.-C., Yeh M.-S., Chiou S.-T., Huang C.-J., Liu T.-Y.;
Genomic structure of galactose-binding protein from the hemolymph of
Taiwanese horseshoe crab.";
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF264067; AAF74773.1;
SEQUENCE 256 AA; 28517 WW; SEC0272B88F44FF8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Eukaryota; Metazoa; Arthropoda; Chellcerata; Merostomata; Xiphosura;
Limulidae; Tachypleus.
NCBI_TaxID=6853;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLRel. 16, Last an
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Pred. No. 13;
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                                                                                                                                  Lamar B., Stoneking T., Stumpf J., Mewes H.W., Lemcke K.,
Mayer K.F.X.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                               EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AFOSB919; AAC13629.1; --
EMBL; AL161472; CABB0878.1; --
MEROPS; C48.001; --
MEROPS; C48.001; --
MEROPS; C48.001; --
INCEPTO: JPR00363; --
INCEPTO: JPR003653; --
                                                                                  Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                    Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein.
SEQUENCE 233 AA; 27632 MW; 46AlE31F70EC86BB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53.2%;
80.0%;
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Best Local Similarity 72...
Best Local Similarity 72...
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                                            STRAIN=CV. COLUMBIA; Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
'`` 8; Conserve
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    [3]
SEQUENCE FROM N.A.
                                                                                                                            SEQUENCE FROM N.A.
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09FWU1
ID 09FWU1
AC 09FWU1
DT 01-MAR:
DT 01-MAR:
DT 01-MAR:
DE HYPOTHI
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STRAIN-CV. NIPPONBARE;
Buell C.R., Yuan Q., Moffat K.S., Hill J.N., Jenkins C.N., Burr P.C.,
Hsiao J., Zismann V., Pai G., Bowman C.L., Fujii C.Y., Vanaken S.E.,
Bowman C.L., Craven B., Utterback T.R., Khalak H., Feldblyum T.V.,
Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
"Oryza sattva chromosome 10 BAC OSJNBa0051D19 genomic sequence.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                   Gaps
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"The Xenopus IP3 receptor: structure, function, and localization in cocytes and eggs.";

Cell 73:555-570(1993).

EMBL; D14400; BAA03304.1; -.

InterPro; IPR000493; -.

InterPro; IPR001682; -.

InterPro; IPR001682; -.

InterPro; IPR003688; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     091908;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
INOSITOL 1,4,5-TRIPHOSPHATE RECRETOR.
Senopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                         Score 41; DB 10; Length 377; Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2693 AA; 306670 MW; CBF6AFFEF16A753C CRC64;
                                                                                                                                                                                                               11 protein.
377 AA; 39255 MW; 28E1C75270877C4D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 2693 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF01365; RYDR ITPR; 1.
PRINTS; PR00779; INSP3RECEPTR.
SMART; SM00472; MIR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                 53.2%;
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Best Local Similarity 57.1.
8; Conservative
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Best Local Similarity 61.5
Matches 8; Conservative
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227 AAASCHASGYVYLH 240
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002240;
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002240
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Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Amanatides P.G., Scherer S.E., In P.W., Hoskins R.A., Galle R.F.,
As George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Button G.G., Wortman J.K., Yandell M.D., Zhang Q., Chen L.X.,
A brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelifer B.D.,
A bril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
B Besson K.H., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
B Besson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolthakov S.,
A Borkova D., Botchan M.K., Bouck J., Brokstein P., Brottler P.,
A Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
A de Pablos B., Delcher A., Deny Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Duyan-Rocha S., Dunkov B.C., Dunn P.,
A Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Felsschmann W.,
A Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                              SEQUENCE FROM N.A.

MEDLINE-99417957; PubMed-10488333;
Tsal C.-C., Kao H.-Y., Yao T.-P., McKeown M., Evans R.M.;
Kao H.-Y., Yao T.-P., McKeown M., Evans R.M.;
SMRTER, a Drosophila nuclear receptor coregulator, reveals that ECR-mediated repression is critical for development.";
Mol. Cell 4:175-186(1999).
EMBL; AF175223; AAD52614.1; -.
ENBBse; FBgn0024308; Smr.
InterPro; IPR000104; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                             Length 3469;
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                                                                                                                                                                                                                                                                                                                                                     364115 MW; 6284E14C5C247CD9 CRC64;
 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAX-2001 (TrEMBLrel. 16, Last annotation update)
SANT DOMAIN PROTEIN SMRTER.
SMR OR SWRIER OR CG4013.
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                             Score 41; DB 5; I
Pred. No. 2.6e+02;
3; Mismatches 1;
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                                                                                                                                                                                                                                                                                   InterPro; IPR002086; -. Pfam; PF00249; myb_DNA-binding; 1.
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                                                                                                                                                                                                                                                                                                                                                                                             53.2%;
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                                                                                                                                                                                                                                                                                                                                                                                          Query Match 53.2
Best Local Similarity 63.6
Matches 7; Conservative
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                                                                                                                                                                                                                                                                     InterPro; IPR001005; -.
                                                                                                                                                                                                                                                                                                                                       SMART; SM00395; SANT; SEQUENCE 3469 AA; 36
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SMR OR CG4013.
01-MAY-2000 (
01-MAY-2000 (
01-MAR-2001 (
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Q9VYJ9
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Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

Hostin D., Houston K.A., Howland T.J., Wei M. H., Ibegwam C.,

Jalai M., Kalush F., Karpen G.H., Kravitz S., Kulp D., Lai Z.,

Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

Mattei B., McIntosh T.C., McIcod M.P., Moshrefi A.,

Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

Nelson D.K.,

Nelson R.N., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

Spier E., Siden Kramos I., Simpson M., Skupski M.P., Smith T.,

Spier E., Spradiing A.C., Stapleton M., Strong R., Sun E.,

Syirskas R., Tector C., Turner R., Venter E., Hang A.H., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,

Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

K. J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheo Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

Scheele S.P. Signis R. Rubin G.M., Venter J.C.;

Reiner 29872185-2195520000.
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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Science 282:2012-2018(1998).
- :- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
- :- SIMILARITY: CONTAINS LIM DOMAIN(S). THE LIM DOMAIN BINDS 2 ZINC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1: Indels
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SEQUENCE 3502 AA; 369068 MW; 74C8004F9DA8F8D9 CRC64;
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Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases
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Last annotation update)
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InterPro; IPR002086; -.
Pfam; PF00249; myb_DNA-binding; 1.
PRIMTS; PR00308; ANTIFREEZEI.
PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE003490; AAF48196.1; -. FlyBase; FBgn0024308; Smr.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Z81054; CAB02885.2;
HSSP; P14859; 1FOG.
InterPro; IPR000047; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEC-3 PROTEIN.
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DR InterPro; IPR001356; -.

DR Pfam; PP000146; homeobox; 2.

DR Pfam; PP000146; homeobox; 2.

DR PRONTS; PR00031; HTHREPRESSR.

DR PROSITE; PS00021; HTMEDBOX_1; 1.

DR PROSITE; PS00021; HOMEOBOX_1; 1.

DR PROSITE; PS00071; HOMEOBOX_2; 1.

DR PROSITE; PS00071; HOMEOBOX_2; 1.

DR PROSITE; PS00071; HOMEOBOX_2; 1.

DR SNART; SM00132; LIM_DOMAIN_1; UNKNOWN_1.

DR SNART; SM00132; LIM, 1.

DR SNART; SM00132; LIM, 1.

DR SNART; SM00132; LIM, 1.

COLETY MART; SM00132; LIM, 1.

A. Inc.

OUETY Match

DR ST.9%; SCORE 40; DB 5; Length 328;

ALIC.

OUETY MATCH

DR ST.9%; SCORE 40; DB 5; Length 328;

ALIC.

OUETY MATCH

DR ST.9%; SCORE 40; DB 5; Length 328;

ALIC.

OUETY MATCH

DR ST.9%; SCORE 40; DB 5; Length 328;

ALIC.

OUETY MATCH

DR ST.9%; SCORE 40; DB 5; Length 328;

DR ST.9%; SCORE 40; DB 5; Le
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Search completed: June 28, 2001, 16:08:27 Job time: 955 sec

: | | | | || : | 194 QVKKEVDAYGYNFEH 208

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

June 28, 2001, 16:14:38 ; Search time 362.28 Seconds (without alignments) 1.171 Million cell updates/sec Run on:

US-09-724-406-30

1 LASNLES 7 Perfect score: Sequence: Title:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

Total number of hits satisfying chosen parameters: 412676 seqs, 60623988 residues

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

Database :

A\_Geneseq\_0601:\*

(SIDSB/)queta/geneseq/)Antise.turi:
(SIDSB/gcgdata/geneseq/panseq/)Antise.turi:
(SIDSB/gcgdata/geneseq/geneseqp/Antise.Dar:\*
(SIDSB/gcgdata/geneseq/geneseqg/geneseqp/Antise.Dar:\*
(SIDSB/gcgdata/geneseq/geneseqg/geneseqg/geneseqp/Antise.Dar:\*
(SID /SIDS8/gcgdata/geneseg/genesegp/AA1980.DAT:\* /SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:\* /SIDS8/gcgdata/geneseg/genesegp/AA1982.DAT:\* 10... 111... 111... 112... 114... 116... 116... 116... 116... Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Мо.

/SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT:\*

CDR2 from murine a H. pylori HSP60-bi GM-CSF receptor al Light chain region VL chain of anti-C Light chain variab Light chain variab Light chain variab Light chain variab Humanised antibody Mouse 23F2G light Description AAR85179 AAR47933 AAW89349 AAW27353 AAY13949 AAR60810 AAR53930 AAR60528 AAR85242 AAW27345 AAB09999 £ Match Length DB 103 107 108 110 1000.0 1000.0 1000.0 1000.0 1000.0 1000.0 Query 100.0 Score 

| Murine 206 antibod<br>Humanised 23F2G 11<br>H. Pylori HSP60-bi<br>Chimeric MAD 9.2.2<br>Human IGE receptor<br>VI region from an<br>Human IGE receptor<br>Light chain variab<br>Light chain variab | nt M   | 44180 666   | 001000   |
|---|--|---|--|
| AAR85236<br>AAW89351<br>AAR10019<br>AAR10539<br>AAR79158<br>AAR79156<br>AAW27358<br>AAW27358<br>AAW27358  |  |   | AAY3954<br>AAR4862<br>AAR4862<br>AAR6517<br>AAR6517<br>AAR3334<br>AAR3334<br>AAR4861 |
| 17<br>20<br>20<br>21<br>12<br>16<br>16<br>18<br>18<br>13  | 20<br>20<br>16<br>22<br>15<br>11               | 115<br>10<br>10<br>10<br>10<br>10<br>10<br>10<br>10<br>10<br>10<br>10<br>10<br>10 | 20<br>15<br>16<br>16<br>17   |
| 111111111111111111111111111111111111111   | 237<br>240<br>260<br>3096<br>215<br>230<br>230 | 230<br>230<br>230<br>87<br>87<br>91<br>110<br>110<br>110                          | 110<br>111<br>111<br>111<br>111<br>121<br>121<br>121                                 |
| 1000.0<br>1000.0<br>1000.0<br>1000.0<br>1000.0<br>100.0<br>100.0  | 100.0<br>100.0<br>100.0<br>93.5<br>93.5        |   | ##########<br>00000000<br>00000000   |
| 31131131131   | 31<br>23<br>23<br>23<br>23                     | 888888888<br>77777777   | 58888888888888888888888888888888888888   |
| 2209874832<br>2009874658433   | 22<br>24<br>25<br>27<br>28                     | 33333333333333333333333333333333333333  | 38<br>9 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4  |

#### ALIGNMENTS

Complementarity determining region; CDR2; murine; mouse; human; high affinity; immunoglobulin E; receptor; monoclonal antibody; IgE; MAb; heavy chain; variable region; humanised; semi-chimeric; chimeric; treatment; prevention; disease; allergy. CDR2 from murine anti-human IgE receptor antibody heavy chain. AAW27345 standard; peptide; 7 AA. 12-DEC-1997 (first entry) AAW27345; AAW27345 RESULT 

Mus spp.

JP09191886-A.

29-JUL-1997

96JP-0024816. 19-JAN-1996; 96JP-0024816. 19-JAN-1996; (ASAK ) ASAHI BREWERIES LTD. (NIKK-) NIKKA WHISKEY KK. (TORI ) TORII YAKUHIN KK.

(TSUR/) TSURA T.

WPI; 1997-429186/40.

Humanised, semi-chimeric and chimeric antibodies against human high-affinity IgE receptor - useful medicinally and have low

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This invention describes a novel method for the detection of a mammalian infection by an acid-resistant microorganism (A) by treating a faecal sample with at least two different monoclonal antibodies (MAD) for their fragments or derivatives) or acomplex (C) between (I) and the corresponding antigen of (A). The first and second (I) bind to epitopes of different antigens (Ag). These epitopes are present, after passage through the intestines, in at least some mammals, and have either: (I) their native structure; or (ii) a structure against which an antibody is produced by an animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Detecting infection by acid-fast microbes for diagnosis of Helicobacter pylori, comprises reacting a faecal sample with two binding reagents for antigens that survive intestinal passage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Acid-resistant microorganism; detection; faecal; intestine; infection; monoclonal antibody; heat shock protein; HSP60; light chain; CDR; complementarity determining region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     H. pylori HSP60-binding antibody light chain CDR2 protein fragment.
                                                                                                                         The present complementarity determining region 2 (CDR2), which is from a murine, anti-human high affinity immunoglobulin E (1gE) receptor, monoclonal antibody (MAD) heavy chain variable region, can be used in the preparation of humanised or semi-chimeric anti-human high affinity IgE receptor MAD. The MAD can be used to treat or prevent diseases, specifically allergies, associated with the receptor. The humanised, semi-chimeric or chimeric MAD have very low antigenicity in humans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 31; DB 18; Length 7; 100.0%; Pred. No. 3.4e+05; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB09999 standard; Protein; 7 AA.
                                                                       Claim 1; Page 12; 26pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 20; Page 20; 84pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98EP-0120517
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 7; Conservative
antigenicity in humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000-365747/31.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200026671-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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infected or immunized with (A), or its extract, lysate, derived protein or fragment, or with a synthetic peptide. Practically all mammals display at least one of the specified epitopes. The method is used to detect infection by acid-fast bacteria, particularly of the genera Helicobacter, Mycobacterium and Campylobacter, specifically H. pylori, H. hepaticus, M. tuberculosis, C. jejuni and C. pylori. (I) may also be used therapeutically. The method is direct and non-invasive, and provides an inexpensive and easily standardizable diagnosis, despite possible degradation of antigens during passage through the intestines. This sequence represents a fragment of a H. pylori heat shock protein, HSP60-binding antibody light chain complementarity determining region CDRI which is used to illustrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present peptide binds the alpha-chain of the GM-CSF receptor, and can therefore be used in binding assays in place of GM-CSF. It can also be used as an antagonist, 1.e. in the treatment of inflammation or autoimmune diseases, or in the prodo. of GM-CSF agonists, i.e. upregulators for the prodo. of immune system cells. The peptide is derived from CDR II of the recombinant antibody light chain analogue of GM-CSF, 23.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      identifying biologically active protein peptide mimics - by prepnof recombinant antibody libraries and synthesising complementary
                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alpha-chain; GM-CSF; receptor; granulocyte; macrophage; colony stimulating factor; binding assay; antegonist; inflammation; autoimmune disease; agonist; upregulator; immune system cell; CDR II; light chain; antibody 23.2.
                                                                                                                                                                                                                                                                                                             100.0%; Score 31; DB 21; 100.0%; Pred. No. 3.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kieber-Emmons T, Von Feldt JM, Weiner DB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GM-CSF receptor alpha-chain binding peptide.
                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 2; Page 49; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR85179 standard; peptide; 17 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   determining region sequences.
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                                                                                                                                                                                                                                                                                                                                                    Conservative
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Matches 7; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-JUN-1996
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                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR85179;
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17 AA;

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10-MAY-1993;
28-FEB-1995;
21-JAN-1997;
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                                                                                                                                                                                                                                                                            29-DEC-1998,
                                                                          AAW89349;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rose LM;
                                                                                                                                                                                                                   Mus sp.
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                                  AAW89349
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                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total RNA was isolated from the hybridoma cell line 23F2G and first strand cDNA was synthesised using the total RNA as a template. The first strand cDNA was used as a template for PCR to obtain double stranded DNA fragments encoding the variable regions of both the heavy and light chains of monoclonal antibody 23F2G. The sequence shown is that of the light chain variable region of MAD 23F2G The humanised form of MAD 23F2G may be administered to alleviate symptoms associated with inflammatory disease states, esp. for the inhibition of inflammatory processes associated with multiple sclerosis. The MAD blocks leukocyte adhesion and migration to inflammatory sites. The MAD is an anti-CD18 integrin sentibody which competes with MAD 60.3 for binding to LFA-1.
                                                                                                                                                                                                                                                                   Amplification; 23F2G; humanised antibody; heavy chain; light chain; hybridoma; inflammation; CD18; human leukocyte integrins; mAb 60.3; monoclonal antibody; LFA-1; adhesion; migration; multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antibodies immunologically reactive with the CD18 of human leukocyte integrins and/or competing with mAb 60.3 for binding to human LFA-1 - for alleviating symptoms associated with inflammatory disease states
                                ö
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Ouery Match

Best Local Similarity 100.0%; Pred. No. 7.8;

Matches 7; Conservative 0; Mismatches 0; Indels (
  16; Length 17;
                                Indels
                               ö
100.0%; Score 31; DB 100.0%; Pred. No. 1;
                            0; Mismatches
                                                                                                                                                     AAR47933 standard; Protein; 103 AA.
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                                                                                                                                                                                                                                           Light chain region of 23F2G.
                                                                                                                                                                                                                                                                                                                                                                                                    93WO-US06734.
                                                                                                                                                                                                                                                                                                                                                                                                                              92US-0915068.
                                                                                                                                                                                                                (first entry)
                            7; Conservative
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              Best Local Similarity
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46 lasnles 52
                                                                       1111111
2 lasnles 8
                                                        1 LASNLES 7
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10-MAY-1993;
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 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rose LM;
                          Matches
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(ATCC HB 11801) and the Chinese hamster ovary (CHO) cell lines 6E6 (ATCC CRL 11398) and B13-24 (ATCC CRL 11397). Monoclonal antibody (MAD) 23F2G (and its humanised variants 6E6 and B13-24) is an anti-human CD18 antibody for the treatment of inflammation, specifically multiple sclerosis. The present sequence is mouse 23F2G light chain variable region from the present invention.
                                                                                                                                                                                                                                  Mouse; humanised; antibody; heavy chain variable region; light chain; 23F2G; inflammatory disease; multiple sclerosis; common beta chain; CD18; human leukocyte integrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hybridomas that secrete anti-CD18 antibody - useful for treating inflammation specifically multiple sclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes the hybridoma cell line 23F2G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 31; DB 20; Length 103; 100.0%; Pred. No. 7.8; ative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Light chain variable region of human CRA2 antibody.
                                                                                                                                                                          Mouse 23F2G light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 6; Column 25-26; 24pp; English.
AAW89349 standard; Protein; 103 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW27353 standard; Protein; 107 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93US-0094535.
92US-0915068.
93US-0060699.
95US-0396089.
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                                                                                                               02-MAR-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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(UNIW ) UNIV WASHINGTON.
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nes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 103 AA;
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AAR60810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Inducer; antibody production; antigen-specific antibody; vaccine; HIV; B-cell activating signal; infectious disease; therapy; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                     The cDNA encoding the present sequence, the light chain variable region of the human antibody (Ab) CRA2, was used in the preparation of a humanised or semi-chimeric monoclonal Ab (MAb), comprising complementarity determining regions (CDR) from a murine, anti-human high affinity immunoglobulin E (IgE) receptor, MAb. The humanised, semi-chimeric or chimeric MAb can be used to treat or prevent diseases, specifically allergies, associated with the receptor, and has very low antigenicity in humans.
Complementarity determining region; CDR; murine; mouse; human; high affinity; immunoglobulin E; receptor; monoclonal antibody; IgE; MAb; light chain; variable region; humanised; semi-chimeric; chimeric; treatment; prevention; disease; allergy; CRA2.
                                                                                                                                                                                                                                                                                                                                                                                                        ó
                                                                                                                                                                                                                  Humanised, semi-chimeric and chimeric antibodies against human high-affinity IgE receptor – useful medicinally and have low
                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 31; DB 18; Length 107; 100.0%; Pred. No. 8.1; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VL chain of anti-CD40 monoclonal antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY13949 standard; Protein; 108 AA.
                                                                                                                                                                                                                                                       Disclosure; Fig 1; 26pp; Japanese.
                                                                                                      96JP-0024816.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98WO-JP04563
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                                                                                                                       96JP-0024816.
                                                                                                                                          BREWERIES LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                         (ASAK ) ASAHI BREWERIES Lī
(NIKK-) NIKKA WHISKEY KK.
(TORI ) TORII YAKUHIN KK.
(TSUR/) TSURA T.
                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity luv...
7; Conservative
                                                                                                                                                                                                                                     antigenicity in humans
                                                                                                                                                                                       WPI; 1997-429186/40.
                                                                                                                                                                                                                                                                                                                                                            107 AA;
                                                                                                                                                                                                 N-PSDB; AAT90024.
                                                                                                                                                                                                                                                                                                                                                                                                                                    1 LASNLES 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W09922008-A1
                                                                                                                       19-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-OCT-1997;
                                                Homo sapiens
                                                                 JP09191886-A
                                                                                                      19-JAN-1996;
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                                                                                   29-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
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                                                                                                                                                                                                                                                                                                                                                             Sequence
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This sequence is the VL chain of an anti-CD40 monoclonal antibody used in the construction of an inducer of the invention.

The inducer is for the production of an antigen-specific antibody with high avidity, consists of a chimeric molecule containing the antigen together with a B-cell activating signal. The inducer is a chimeric molecule containing: (1) an antigen portion recognised by a B-cell antigen receptor; and (2) a signal transmitter portion, such as anti-CD40 antigen receptor; and (2) a signal transmitter portion, such as anti-CD40 antigen-specific antibody. The inducer may be incorporated into a vaccine for prevention and treatment of infectious diseases including HIV, and used to produce antigen-specific monoclonal antibodies for the treatment, diagnosis and investigation of diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                     Inducer for production of antigen-specific antibody of high avidity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antibody; humanised antibody; variable region; immune response; cytomegalovirus; glycoprotein; complementarity determining region; CDR; heavy chain; light chain; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New humanised monoclonal antibodies against Human Cytomegalovirus - contain murine CDR and human framework modified to increase specificity or affinity, for treatment or prevention of HCMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ó
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Light chain variable region of antibody HCMV16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Figure 2; 53pp; English.
                                                                                                                                                                                                                                                                            Example; Page 29-30; 36pp; Japanese.
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(SUME ) SUMITOMO ELECTRIC IND CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (KETT-) KETTOCK LODGE CAMPUS 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92GB-0021654.
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Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1994-151321/18.
                                                                                                                                  WPI; 1999-303020/25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 108 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAQ73749
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-DEC-1994
                                                                          Sakaguchi N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR60810;
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Human monoclonal antibodies may be made specific for a pathogen by susbtituting the complementarity determining regions (CDR's) from the murine antibody variable domains which show desirable binding properties to that pathogen, into the human immunoglobulin heavy and light chain variable domains. These "humanised" antibodies should elicit a considerably reduced immune response in humans compared to chimeric antibodies as they contain considerably less murine components and their half life in the circulariby abould approach that of natural human antibodies. This sequence is taken from a donor monoclonal antibody HCMV16, specific for the human cytomegalovirus gH glycoprotein from which CDR's were taken to construct humanised antibodies. Humanised antibodies are described in AAQ63902-063908.
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Sequence 110 AA;

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100.0%; Score 31; DB 15; Length 110; 100.0%; Pred. No. 8.4; cive 0; Mismatches 0; Indels (
Query Match
Best Local Similarity 100...
                                                                                      54 lasnles 60
                                                             1 LASNLES 7
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AAR53930 standard; Protein; 111 AA. 05-DEC-1994 (first entry) AAR53930; 6

Antibody; humanised antibody; variable region; immune response; cytomegalovirus; glycoprotein; complementarity determining region; CDR; heavy chain; light chain. Light chain variable region of humanised antibody 16HuVK. A STATE OF S

Mus musculus Homo sapiens

WO9409136-A.

28-APR-1994.

93WO-GB02134. 15-OCT-1993;

92GB-0021654. 15-OCT-1992;

(KETT-) KETTOCK LODGE CAMPUS 2.

Carr FJ, Hamilton AA, Harris WJ;

WPI; 1994-151321/18. N-PSDB; AAQ63908 New humanised monoclonal antibodies against Human Cytomegalovirus - contain murine CDR and human framework modified to increase specificity or affinity, for treatment or prevention of HCMV infection

Example 1; Figure 5; 53pp; English.

Human monoclonal antibodies may be made specific for a pathogen by subblituting the complementarity determining regions (CDR's) from the murine antibody variable domains which show desirable binding properties to that pathogen, into the human immunoglobulin heavy and light chain variable domains. These "humanised" antibodies should elicit a considerably reduced immune response in humans compared to chimeric antibodies as they contain considerably less murine components and their half life in the circulation should approach

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that of natural human antibodies. This sequence is a humanised heavy chain variable region comprising CDR's from the donor monoclonal antibody HCMV16, specific for the human cytomegalovirus gH glycoprotein. The framework region of the human heavy chain has been modified. Humanised antibodies are described in AAQ63902-Q63908.
                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                            ö
                                                                                                                                                                       Length 111;
                                                                                                                                                                                                            Indels
                                                                                                                                                                     100.0%; Score 31; DB 15;
100.0%; Pred. No. 8.5;
Live 0; Mismatches 0;
                                                                                                                                                                                                            Conservative
                                                                                                                                                                                          Local Similarity
les 7; Conser
                                                                                                                  111 AA;
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. 1 LASNLES 7

54 lasnles 60

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RESULT 10 AAR60528

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Gaps

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AAR60528 standard; Protein; 111 AA.

AAR60528;

07-APR-1995 (first entry)

Light chain variable region of monoclonal antibody 5E8.

Secretion sequence; vector; antibody; single chain antibody; promoter; Bacillus subtilis; ss.

Synthetic.

EP614982-A.

14-SEP-1994.

94EP-0200564. 05-MAR-1994; 93IT-0MI0456. 10-MAR-1993;

(ENIE ) ENIRICERCHE SPA.

Tortora O, Tosi C; Cuzzoni A, De FERRA F, Grandi G,

WPI; 1994-281209/35. NAME OF COLORD C

N-PSDB; AAQ71286.

Vector for secretion of single chain antibody from Bacillus subtilis - conty. neutral protease promoter and specific leader sequence, providing high yield of soluble antibody for diagnostic therapeutic use

Example 3; Figure 2; 27pp; English.

The sequence encoding the variable region of the light chain of the monoclonal antibody 5E8 (specific for the alpha subunit of human gonadotrophin) was amplified for its use in a recombinant vector which also comprised (1) the promoter of the gene for the neutral protease of Bacillus subtlins BGSC 1A341, (2) the secretion sequence described in AAQ71278. The amplified fragment was used to produce a DNA sequence encoding an antibody in single molecule form with the sequence VH/VK-L-VK/VH-(TAG)n, where VH and VK are the variable regions of the heavy and light chains of the antibody and L is the linker of sequence Val-Ser-Ser-(G1Y(4)-Ser)3, TAG is a peptide incomplised by polyclonal antibodies directed towards the same peptide, is 10 of The vector is used for the production of single chain antibodies which have improved pharmacokinetic properties and can be produced more economically than monoclonal antibodies. The vector callows production of antibodies in completely soluble form with

111 AA; Seguence AAR85236 standard; Protein; 111 AA.

RESULT 12

AAR85236

(first entry)

05-APR-1996

AAR85236;

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                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Varicella zoster virus gpIII antibody with humanised variable region - for treatment, prevention or diagnosis of varicella zoster virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antibody; varicella zoster virus; Ab; VSV; treatment; prevention; infection; detection; isolation; monoclonal antibody; MAb; mimetic; humanised; murine; heavy chain; light chain; variable region; CDR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antibodies (Ab) comprising a humanised variable region specifically
                                                                                     ;
0
                               Length 111;
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                                                                                     Indels
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                         100.0%; Score 31; DB 15;
100.0%; Pred. NO. 8.5;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                AAR85242 standard; Protein; 111 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95WO-US05305.
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Query Match
Best Local Similarity 100...
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Varicella zoster virus gpIII antibody with humanised variable region - for treatment, prevention or diagnosis of varicella zoster virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 respectively. The framework may include at least one mutation that improves binding specificity or affinity. The heavy and light chain variable regions are preferably (VZVHu-VH, -VHKRIIS, -VHTLY, -VHKVRSE or -VHS) and VZVHuVK respectively.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                     Antibody; varicella zoster virus; Ab; VSV; treatment; prevention; infection; detection; isolation; monoclonal antibody; MAb; mimetic; humanised; murine; heavy chain; light chain; variable region; CDR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antibodies (Ab) comprising a humanised variable region specifically binding to a varicella zoster virus (VZV) can be used to treat or prevent VZV infection. They may optionally be attached to a therapeutic agent. They may also be used, when labelled, to detect NZV particles and infected cells in blood; for the removal neutralisation of infectious VZV in blood; for the selection/isolation of human monoclonal Abs and for the design of (non-peptide mimetics with similar diagnostic and therapeutic uses. The variable region CDR portion is derived from murine Ab 206 and the heavy and light chain variable region frameworks are NEWM and REI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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                                                                          Murine 206 antibody variable light chain region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Moss MT, Wallace TP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SCOT-) SCOTGEN BIOPHARMACEUTICALS INC.
                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; Figure 2; 58pp; English.
                                                                                                                                                                                                                                                     54..60
/label= CDR 2.
93..101
                                                                                                                                                                                                                                24..38
/label= CDR 1.
                                                                                                                                                                                                                                                                                            93..101
/label= CDR 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carr FJ, Harris WJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1996-010932/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 111 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAT06051.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54 lasnles 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 LASNLES 7
                                                                                                                                                                                   Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                  28-APR-1995;
                                                                                                                                                                                                                                Binding-site
                                                                                                                                                                                                                                                                                           Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                28-APR-1994;
                                                                                                                                                                                                                                                              Binding-site
                                                                                                                                                                                                                                                                                                                                       W09531546-A1
                                                                                                                                                                                                                                                                                                                                                                     23-NOV-1995.
                                                                                                                                                        NEWM; REI.
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Gaps

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0; Indels

Query Match
100.0%; Score 31; DB 17; Length 111;
Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 7; Conservative 0; Mismatches 0; Indels (

1 LASNLES 7

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H. pylori HSP60-binding antibody light chain protein.
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                                                                                                                                  WO200026671-A1
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                                                                                                Unidentified
                                                                                                                                                                                                              29-OCT-1999;
                                                                                                                                                                                                                                                                    06-NOV-1998;
                                                                                                                                                                        11-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                      Ringeis A;
                                                                                                                                                                                                                                                                                                                                              Reiter C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR10539;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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AAR10539
XX
AC AAR105:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes the hybridoma cell line 23F2G (ATCC HB 11801) and the Chinese hamster covary (CHO) cell lines 6E6 (ATCC CRL 11399) and B13-24 (ATCC CRL 11397). Monoclonal antibody (MAD) 23F2G (and its humanised variants 6E6 and B13-24) is an anti-human CD18 antibody for the treatment of inflammation, specifically multiple sclerosis. The present sequence represents humanised 23F2G light chain variable region from the present invention.
                                                                                                                                                                                                                        Mouse; humanised; antibody; heavy chain variable region; light chain; 23F2G; inflammatory disease; multiple sclerosis; common beta chain; CD18; human leukocyte integrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hybridomas that secrete anti-CDI8 antibody - useful for treating inflammation specifically multiple sclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 31; DB 20; Length 111; 100.0%; Pred. No. 8.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                  Humanised 23F2G light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 6; Column 27-30; 24pp; English.
                                                                    AAW89351 standard; Protein; 111 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB10019 standard; Protein; 111 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93US-0094535.
92US-0915068.
93US-0060699.
95US-0396089.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            97US-0785571
                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.

Best Local Similarity 100.

Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ICOS-) ICOS CORP.
(UNIW ) UNIV WASHINGTON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-094920/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAV81909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 LASNLES 7
                                                                                                                                                                                                                                                                                                                        sapiens.
                                                                                                                                              02-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-JUL-1992;
10-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-FEB-1995;
21-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                US5854070-A
                                                                                                                                                                                                                                                                                                                                                                                                                    29-DEC-1998
                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                        AAW89351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB10019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rose LM;
                                                                                                                                                                                                                                                                                                      Mus sp.
                                RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 1
                                                AAW89351
                                                                                      SAXAXEX
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This invention describes a novel method for the detection of a mammalian infection by an acid-resistant microorganism (A) by treating a faecal sample with at least two different monoclonal antibodies (MAD) (or their cample with at least two different monoclonal antibodies (MAD) (or their cragments or derivatives) or aptamers (collectively (I)) and detecting formation of a complex (C) between (I) and the corresponding antigen of (A). The first and second (I) bind to epitopes of different antigens (A). These epitopes are present, after passage through the intestines, in at least some mammals, and have either: (i) their native structure; or (ii) a structure against which an antibody is produced by an animal infection of with a synthetic peptide. Practically all mammals display at least one of the specified epitopes. The method is used to detect infection by acid-fast bacteria, particularly of the genera Helicobacter, Mycobacteriun and Campylobacter, specifically H. Pylori, H. hepaticus, M. tuberculosis, C. jejuni and C. pylori. (I) may also be used therapeutically. The method is direct and non-invasive, and provides an inexpensive and easily standardizable diagnosis, despite possible sequence represents the H. Pylori hast shock protein, HSPGO-binding antibut (A) and the standardizable diagnosis, despite the method is a conting passage through the intestines. This sequence represents the H. Pylori hast shock protein, HSPGO-binding and the diagnosis and provides and p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Detecting infection by acid-fast microbes for diagnosis of Helicobacter pylori, comprises reacting a faecal sample with two binding reagents for antigens that survive intestinal passage
Acid-resistant microorganism; detection; faecal; intestine; infection; monoclonal antikody; heat shock protein; HSP60; light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Friedrichs U, Heppner P, Lakner M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 31; DB 21; 100.0%; Pred. No. 8.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chimeric MAb 9.2.27 light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR10539 standard; Protein; 112 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Fix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 1; 84pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98EP-0120517.
98EP-0120687.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-EP08212.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-APR-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best_Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cullmann G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CONN-) CONNEX GMBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-365747/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 111 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAA40199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of the invention
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This sequence is encoded by recombinant DNA contained in vector PTZK910. This is ligated to a DNA sequence encoding a human light (L) chain constant (C) region, in the construction of pG9.2.72K. This vector is used to transform host cells, in conjunction with vector pN9.2.27G1 contg. murine heavy (H) chain variable (V) region and human heavy chain C region. The resulting host cell expresses the chimeric antibody 9.2.27 which is directed against proteoglycans of human melanoma cells. This chimeric monoclonal antibody (MAD) is useful in the diagnosis and treatment of melanoma. The use of human C-regions avoids the problems associated with murine monoclonals e.g. see also AAQ10380-84.
               Chimeric antibodies; human glycoprotein antigen; melanoma; cancer;
                                                                                                                                                                                                                                                                                                                      Monoclonal antibody contg. recombinant DNA - binds to human chondroitin sulphate proteoglycan on melanoma cells for melanoma treatment and diagnosis
                                                                                                                                                                                                                                           Gadski RA;
                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; page 17; 33pp; English.
                                                                                                                                              90EP-0308402.
                                                                                                                                                                             89US-0387665.
                                                                                                                                                                                                            (ELIL ) ELI LILLY & CO.
                                                                                                                                                                                                                                           Beavers LS, Bumol TF,
                                                                                                                                                                                                                                                                       WPI; 1991-038771/06.
N-PSDB; AAQ10379.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112 AA;
                                               Mus musculus.
                                                                                                                                              31-JUL-1990;
                                                                                                              06-FEB-1991.
                                                                              EP411893-A.
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Gaps ; 0 Query Match ' 100.0%; Score 31; DB 12; Length 112; Best Local Similarity 100.0%; Pred. No. 8.5; Matches 7; Conservative 0; Mismatches 0; Indels 1 LASNLES 7 δλ

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Search completed: June 28, 2001, 16:14:39 Job time: 1327 sec

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June 28, 2001, 16:01:15 ; Search time 138.34 Seconds (without alignments) 1.019 Million cell updates/sec
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                            OM protein - protein search, using sw model
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31
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                                                                                                                                                                                                                  Perfect score:
                                                                                                                                                                                                                                    Sequence:
                                                                                                                 Run on:
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Total number of hits satisfying chosen parameters:

193259 seqs, 20144635 residues

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

/cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*
/cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*
/cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*
/cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*
/cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*
/cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\* Issued\_Patents\_AA:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Description                   | . 2             |       | Seguence 4, Appli<br>Seguence 86, Appl | 86.              | Sequence 25, Appl | 25,              | 49,              | 2, 4            | 7               | 7                | Sequence 30, Appl | 32,              | Ξ                | 14,              | 30,              | 32,              | 30,               | 32,               | 18,              | 22,              | 18,              | 22,              | 17.               | 18                | 22,               | 4,               |
|-------------------------------|-----------------|-------|--|------------------|-------------------|------------------|------------------|-----------------|-----------------|------------------|-------------------|------------------|------------------|------------------|------------------|------------------|-------------------|-------------------|------------------|------------------|------------------|------------------|-------------------|-------------------|-------------------|------------------|
| ID                            | US-08-712-212-5 | 08-90 | US-08-137-117D-86                      | US-08-436-717-86 | US-08-137-117D-25 | US-08-436-717-25 | US-08-273-146-49 | US-08-017-570-2 | US-08-471-426-2 | PCT-US94-01709-2 | US-08-111-080-30  | US-08-111-080-32 | US-08-275-053-11 | US-08-275-053-14 | US-08-211-980-30 | US-08-211-980-32 | PCT-US93-07967-30 | PCT-US93-07967-32 | US-08-111-080-18 | US-08-111-080-22 | US-08-211-980-18 | US-08-211-980-22 | PCT-US92-07111-17 | PCT-US93-07967-18 | PCT-US93-07967-22 | US-08-462-467B-4 |
| рв                            | 77              | ٦ -   | · ~                                    | 7                | ~                 | ~                | ~                | -               | Н               | 'n               | -                 | ٦                | Н                | -                |                  |                  | ഹ                 | S                 | -4               | Н                | Н                | Н                | S                 | Ŋ                 | Ŋ                 | 4                |
| %<br>Query<br>Match Length DB | 17              | 111   | 130                                    | 130              | 131               | 131              | 91               | 110             | 110             | 110              | 111               | 111              | 111              | 111              | 111              | 111              | 111               | 111               | 121              | 121              | 121              | 121              | 121               | 121               | 121               | 1618             |
| %<br>Query<br>Match           | 100.0           | 100.0 | 100.0                                  | 100.0            | 100.0             | 100.0            | 90.3             | 90.3            | 90.3            | 90.3             | 90.3              | 90.3             | 90.3             | 90.3             | 90.3             | 90.3             | 90.3              | 90.3              | 90.3             | 90.3             | 90.3             | 90.3             | 90.3              | 90.3              | 90.3              | 90.3             |
| Score                         | 31              | 31    | 31                                     | 31               | 31                | 31               | 28               | 28              | 28              | 28               | 28                | 28               | 28               | 28               | 28               | 28               | 28                | 28                | 28               | 28               | 28               | 78               | 28                | 28                | 28                | 28               |
| Result<br>No.                 | 1,0             | ı m   | 4                                      | ഗ                | 9                 | 7                | <b>30</b> (      |                 | 01              | Ξ:               | 12                | 13               | 14               | 15               | 16               | 17               | 18                | 19                | 20               | 77               | 22               | 23               | 24                | 25                | 56                | 27               |

Score 31; DB 2; Length 17; Pred. No. 0.47;

100.0%; 100.0%;

Query Match Best Local Similarity

| Sequence 2. Appli | œ                | 137                | Sequence 137, App | Sequence 16, Appl | Sequence 18, Appl | Sequence 18, Appl | Sequence 40. Appl | 9               | 10                | 26.              | 26.              | , A             |                 | 20.               |                 | 46.              | Sequence 47, Appl |  |
|-------------------|------------------|--------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-----------------|-------------------|------------------|------------------|-----------------|-----------------|-------------------|-----------------|------------------|-------------------|--|
| US-08-462-467B-2  | US-08-462-467B-8 | US-08-137-117D-137 | US-08-436-717-137 | US-08-318-970B-16 | US-08-483-636-18  | US-08-483-632-18  | US-08-767-128-40  | US-08-984-277-6 | US-08-765-179B-10 | US-08-202-047-26 | US-08-964-690-26 | US-08-466-151-6 | US-08-442-542-8 | US-08-483-749A-20 | US-08-765-469-8 | US-07-634-278-46 | US-07-634-278-47  |  |
| 4                 | 4                | -                  | ~                 | ٦                 | ~                 | ~                 | 4                 | ٣               | ~                 | Н                | ٣                | m               | Н               | m                 | m               | -                | -                 |  |
| 2887              | 2887             | 9                  | 9                 | 7                 | 7                 | 7                 | 37                | 41              | 64                | 106              | 106              | 106             | 110             | 110               | 110             | 111              | 111               |  |
| 90.3              | 90.3             | 87.1               | 87.1              | 87.1              | 87.1              | 87.1              | 87.1              | 87.1            | 87.1              | 87.1             | 87.1             | 87.1            | 87.1            | 87.1              | 87.1            | 87.1             | 87.1              |  |
| 28                | 28               | 27                 | 27                | 27                | 27                | 27                | 27                | 27              | 27                | 27               | 27               | 27              | 27              | 27                | 27              | 27               | 27                |  |
| 28                | 58               | 30                 | 31                | 32                | 33                | 34                | 35                | 36              | 37                | 38               | 39               | 40              | 41              | 42                | 43              | 44               | 45                |  |

### ALIGNMENTS

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GENERAL INFORMATION:
APPLICANT: Williams, William V.
APPLICANT: Kieber-Emmons, Thomas
APPLICANT: Weiner, David B.
APPLICANT: VonFeldt, Joan M.
TITLE OF INVENTION: Blologically active peptides and
TITLE OF INVENTION: methods of identifying the same
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/712,212
FILING DATE: 03-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                      ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz 6
ADDRESSEE: No. 5837460ris
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/235,404
FILING DATE: 29-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UPN-1554
                       ; Sequence 5, Application US/08712212; Patent No. 5837460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: UPN-:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: protein US-08-712-212-5
                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linəar
                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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us-08-712-212-5
                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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RECOMBINANT VECTOR AND USE THEREOF FOR EXOCELLULAR PREPARATION OF SINGLE MOLECULA ANTIBODIES FROM BACILLUS SUBTILIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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APPLICANT: CUZZONI, ANNA
TITLE OF INVENTION: RECOMBINANT VECTOR AND USE THEREOF FOR
TITLE OF INVENTION: EXCELLULAR PREPARATION OF SINGLE MOLECT
TITLE OF INVENTION: BACILLUS SUBTILIS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
STREET: ALINGTON
STREET: VIGINIA
COUNTRY: U.S.A.
ZIP: 2220-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: SATO, Koh
APPLICANT: BENDIG, Mary
APPLICANT: BENDIG, Mary
APPLICANT: SALDANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 31;
100.0%; Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 2264-061-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                        омВЕК: US/08/207,169A
08-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 86, Application US/08137117D; Patent No. 5795965; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5674712man F.
REGISTRATION NUMBER: 24,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , MOLECULE TYPE: protein US-08-207-169A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 3000 ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 08
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| 54 LASNLES 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , 1 LASNLES 7
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US-08-137-117D-86
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                                                              Gaps
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                                                                                                                                                                                                                                    Sequence 5, Application PC/TUS9505160
GENERAL INFORMATION:
APPLICANT: Williams, William V.
APPLICANT: Weiner, David B.
APPLICANT: Weiner, David B.
TILE OF INVENTION: Biologically active peptides and TITLE OF INVENTION: methods of identifying the same NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: Norris
                                                              Indels
                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : One Liberty Place, 46th Floor Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordberfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: UPN-2245
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3100
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/08207169A; Patent No. 5674712; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
61LING DATE: 29-APR-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NEGRADIO, GUIDO
DE FERRA, FRANCESCA
TOSI, CLAUDIO
TORTORA, ORNELLA
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LENGTH: 17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.

Best Local Similarity 100.

Matches 7; Conservative
                                                              7; Conservative
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2 LASNLES 8
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                                                                                                   1 LASNLES 7
                                                                                                                            2 LASNLES 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: US
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US-08-207-169A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
                                                                                                                                                                                                  RESULT 2
PCT-US95-05160-5
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                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 6
US-08-137-117D-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: SATO, Koh
APPLICANT: BENDIG, Mary
APPLICANT: SALDANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,717
                                                        CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                         NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/126/AAOK
TELECOMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UMBER: WO PCT/JP92/00544
24-APR-1992
                   APPLICATION NUMBER: US/08/137,117D
FILING DATE: 20-DEC-1993
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: WO PCT/JP92/00
FILING DATE: 24-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-436-717-86
Sequence 86, Application US/08436717
Patent No. 5817790
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 904136
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Floppy disk
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: protein US-08-137-117D-86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73 LASNLES 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: SATO, Koh
APPLICANT: BENDIG, Mary
APPLICANT: SCEVEN
APPLICANT: SALDANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: 10TBREGUKIN-6 RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117D
FILING DATE: 20-DEC-1993
CLASSIFICATION NUMBER: US/08/137,117D
FILING DATE: 24-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 4-32084
FILING DATE: 19-FEB-1992
PROR APPLICATION NUMBER: UP 3-95476
FILING DATE: 25-APR-1991
ATFORNEY/AGENT INPOMBER: UP 3-95476
FILING DATE: 25-APR-1991
ATFORNEY/AGENT INPOMBER: 25,258
REGISTRATION NUMBER: 25,258
                                                                                                                                                *** SEPERATION NUMBER: 25,258

**** REFERENCE/DOCKET NUMBER: 53466/126/AAOK

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300

TELEX: 904136

INFORMATION FOR SEQ ID NO: 86:

SEQUENCE CHARACTERISTICS:

LENGTH: 130 amino acids

TOPOLOGY ''
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Foley & Lardner
3000 K Street, N.W., Suite 500
APPLICATION NUMBER: JP 4-32084.
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATOMNEY/AGENT INFORMATION:
NAME: WEGISTRATION NUMBER: 25,258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 25, Application US/08137117D
; Patent No. 5795965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-436-717-86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA ZIP: 20007-5109 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Washington
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LENGIH: 131 amino acids
          TOPOLOGY: line
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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74 LASNLES 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 LASNLES 7
                                                                                                                                                                                                                  1 LASNLES 7
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                                                                                                                                                                                                                                                                                                             RESULT 8
US-08-273-146-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: MI
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
                                                                                                                                                                                                                                                                                                                                                                           Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qq
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                                                                                                                                                                                                                                                                      100.0%; Score 31; DB 1; Length 131; 100.0%; Pred. No. 4.8; or Indels ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INCURALION:
APPLICANT: TSCCHIXA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: SATO, Koh
APPLICANT: BENDIG, Mary
APPLICANT: JONES, Steven
APPLICANT: SALDANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA RELEASE #1.0, VERSION #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING MARE: 19-FEB-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117

FILING DATE: 20-DEC-1993

APPLICATION NUMBER: W0 PCT/JP92/00544

FILING DATE: 24-APR-1992

PRIOR APPLICATION DATA: UP 4-32084

FILING DATE: 19-FEB-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53466/126/AAOK
  REFERENCE/DOCKET NUMBER: 53466/126/AAOK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 19 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 25, Application US/08436717
Patent No. 5817790
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/POCKET NUMBER: 5346(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5390
TELEFAX: (202)672-5399
                TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: 904136
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100...
                                                                                                                                                                         TOPOLOGY: 11near

MOLECULE TYPE: protein

US-08-137-117D-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 20007-5109
                                                                                                                                                                                                                                                                                                                                                                                           74 LASNLES 80
                                                                                                                                                                                                                                                                                                                                                       1 LASNLES 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 7
US-08-436-717-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Smith, Rodger
APPLICANT: McCafferty, John
APPLICANT: Chiswell, David
APPLICANT: Chiswell, David
APPLICANT: Titsgerald, Kevin
APPLICANT: Fitzgerald, Kevin
APPLICANT: Kenten, John H.
APPLICANT: Martin, Mark T.
APPLICANT: Titmas, Richard C.
APPLICANT: Williams, Richard C.
APPLICANT: Williams, Richard O.
TITLE OF INVENTION: The Isolation and Production of
TITLE OF INVENTION: Catalytic Antibodies using Phage Technology
                                                                                           Ouery Match 100.0%; Score 31; DB 2; Length 131; Best Local Similarity 100.0%; Pred. No. 4.8; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NDATA:
APPLICATION NUMBER: US/08/273,146
FILING DATE: 14-JUL-1994
APPLICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 28; DB 2;
Pred. No. 15;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: GERV, Inc.
STRREET: 1530 East Jefferson St:
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                   Sequence 49, Application US/08273146 Patent No. 5855885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: RYAN, JOHN W.
REGISTRATION NUMBER: 33,771
REFERENCE/DOCKET NUMBER: 099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-984-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 49: SEQUENCE CHARACTERISTICS: LENGTH: 91 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90.3%;
85.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: protein US-08-273-146-49
; MOLECULE TYPE: protein US-08-436-717-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 6; Conserva
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Sequence 2, Application US/08471426

Sequence 2, Application US/08471426

Septent No. 5808033

GENERAL INFORMATION:
APPLICANT: GOURLIE, BRIAN B

APPLICANT: RIXON, MARK W

APPLICANT: RAPLAN, DONALD A

APPLICANT: SCHLOM, JEFFREY

TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC

TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:
                                                                                                   APPLICANT: GOURLIE, BRIAN B
APPLICANT: RIXON, MARK W
APPLICANT: RIXON, PEFER S
APPLICANT: KAPLAN, DONALD A
APPLICANT: SCHLOM, JEFFREY
TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 28; DB 1; Length 110;
Pred. No. 18;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: US

COUNTRY: US

ZIP: 48641-1967

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/017,570
FILING DATE: 19930216
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: ULABR: DATABE
REFIGENCE/DOCKET NUMBER: C-38,777
TELEPHONICATION INFORMATION:
TELEPHONE: (517) 636-8104
INFORMATION FOR SEQ ID NO: 2:
CPONTENCE CHARRACTERISTICS:
                                        Sequence 2, Application US/08017570 Patent No. 5472693 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: P.O. Box 1967
CITY: Midland
                                                                                                                                                                                                                                                                                                   ADDRESSEE: Duane C. Ulmer
STREET: P.O. Box 1967
CITY: Midland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 90.3%;
Best Local Similarity 85.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-08-017-570-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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54 LASNLQS 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
RESULT 9
US-08-017-570-2
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GENERAL INFORMATICN:
APPLICANT: THE DOW CHEMICAL COMPANY
APPLICANT: THE DOW CHEMICAL COMPANY
APPLICANT: THE DOW CHEMICAL COMPANY
APPLICANT: U.S.A. DEPT. OF HEALTH AND HUMAN SERVICES
TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: DUANE C. Ulmer
STREET: P.O. Box 1967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 28; DB 1; Length 110;
Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,426
FILING DATE: 06-JUN 1995
CLASSIFICATION 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/017,570
FILING DATE: 16-FEB-1993
ATTONEY/AGENT INPORMATION:
NAME: ULMER, DUANE C
REGISTRATION NUMBER: 34,941
REFERENCE/DOCKET NUMBER: C-38,777
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 110 emaino acids
TYPE: amaino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: US

ZIP: 48641-1967

ZIP: 48641-1967

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATCHIT Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/01709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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NAME: ULMER, DDANE C
REGISTRATION NUMBER: 34,941
REFERENCE/DOCKET NUMBER: 38
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90.3%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (517) 636-8104 INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 85./*,
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-471-426-2
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Midland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 LASNLES 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: MI
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PCT-US94-01709-2
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US-08-111-080-32
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                                                                                                           Gaps
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0
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                                                                  Score 28; DB 5; Length 110; Pred. No. 18;
                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Ohno, Tsuneya
APPLICANT: Ohno, Tsuneya
TTLE OF INVENTION: HIV Immunotherapeutics
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/111,080
                                                                                                                                                                                                                                                                                                                                                                                                                            : 6300 Sears Tower, 233 S. Wacker Drive
Chicago
Illinois
                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION: 424
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 07/748,562
FILING DATE: 22-AUG-1991
FILING DATE: 24-AUG-1992
PRIOR APPLICATION NUMBER: PCT/US92/07111
FILING DATE: 24-AUG-1992
PRIOR APPLICATION NUMBER: 22-APR-1993
ATORNEY,AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 31629
TELECOMMUNICATION INFORMATION:
TELEPAN: (312) 474-6300
TELEFAN: (312) 474-6448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                               Sequence 30, Application 08/111080
Patent No. 5558865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Borun, Michael F. REGISTRATION NUMBER: 25,447
                                                                      90.3%;
85.7%;
                                                 Query Match
Best Local Similarity 85./~,
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 111 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: protein US-08-111-080-30
; MOLECULE TYPE: protein PCT-US94-01709-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 6; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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60606
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                                                                                                                                          1 LASNLES 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                  US-08-111-080-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE:
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Sequence 11, Application US/08275053
Patent No. 5607847
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Virus antibody.
TITLE OF INVENTION: Virus antibody.
NUMBER OF SEQUENCES: 16
COMPUTER READABLE FORM:
MEDIUM YFPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90.3%; Score 28; DB 1; Length 111;
85.7%; Pred. No. 19;
Live 1; Mismatches 0; Indels
                                                                                                                                                          ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Borun
                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDICH TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/111,080
                                                                                                                                                                                                           6300 Sears Tower, 233 S. Wacker Drive
                                                           APPLICANT: Ohno, Tsuneya
TITLE OF INVENTION: HIV Immunotherapeutics
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 22-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/07111
FILING DATE: 24-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION DATE: US 08/039,457
FILING DATE: 22-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: BOTION MICHAEL F.
REGISTRATION NUMBER: 25,447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILLING DATE: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/748,562
FILING DATE: 22-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-6448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
Sequence 32, Application 08/111080
Patent No. 5558865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 310
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 90.3
Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-111-080-32
                                                                                                                                                                                                                              CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :||||||
54 VASNLES 60
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US-08-275-053-11
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US-08-275-053-14

Sequence 14, Application US/08275053

Patent No. 5607847

GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Virus antibody.
TITLE OF INVENTION: Virus antibody.
TITLE OF INVENTION: Virus antibody.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
APPLICATION NUMBER: US/08/275,053
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/01798
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: ADSOLUTE TOWN NUMBER: DESCOURCE TYPE: TOPPOLOGY: Innear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
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SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/275,053
PRIOR APPLICATION NUMBER: US/08/275,053
FROM ATTON DATA:
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHRRACTERISTICS:
ILENGTH: 111 amino acids
TYPE: amino acid
STRANDEDNESS: single
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-275-053-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 90.3%; Score 28; DB 1; Length 111; Best Local Similarity 85.7%; Pred. No. 19; Matches 6; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                           Score 28; DB 1; Length 111;
Pred. No. 19;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: June 28, 2001, 16:01:15
Job time: 523 sec
                                                                                                                                                                                                                                                                                                                                                             Query Match 90.3%;
Best Local Similarity 85.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: protein US-08-275-053-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :111111
54 VASNLES 60
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54 VASNLES 60
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

June 28, 2001, 15:58:46 ; Search time 234.85 Seconds (without alignments) 2.270 Million cell updates/sec Run on:

US-09-724-406-30 Title:

1 LASNLES 7 Perfect score: Sedneuce:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 seqs, 76174552 residues Searched:

219241 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

PIR\_68:\* Database :

1: piri:\* 2: pir2:\* 3: pir3:\* 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Description              | Iq kappa chain V r | light  | kappa  |        | kappa  | i-qlyc | ~      |        | kappa chain | nociona | myosin heavy chain | cutinase (EC 3.1 |        | heavy  |        | myosin heavy chain | heavy  |        | hypothetical prote |        |        | hypothetical prote | hypothetical prote | a      | hypothetical prote |        | •-     | Ig kappa chain V r | kappa  |
|--------------------------|--------------------|--------|--------|--------|--------|--------|--------|--------|-------------|---------|--------------------|------------------|--------|--------|--------|--------------------|--------|--------|--------------------|--------|--------|--------------------|--------------------|--------|--------------------|--------|--------|--------------------|--------|
| ID                       |                    | PH1076 | KVMS84 | KVMS75 | KVMS40 | D45722 | S45715 | KVMSM6 | A56169      | JC5810  | PS0349             | UVFUS            | S39082 | S39083 | S24348 | JX0178             | A29320 | S42193 | H75004             | A71158 | 568241 | T28892             | T19266             | S63397 | B64234             | S50705 | C38601 | B38601             | S25462 |
| DB                       | N                  | 7      | ~      | -      | Н      | ~      | 7      | П      | 7           | 7       | ~                  | Н                | 7      | ~      | 7      | -                  | 7      | 7      | ~                  | ~      | ~      | 7                  | ~                  | ~      | Н                  | 7      | 7      | 7                  | 7      |
| Query<br>Natch Length DB | 95                 | 102    | 111    | 111    | 111    | 111    | 112    | 131    | 210         | 218     | 94                 | 230              | 741    | 936    | 955    | g,                 | 1940   | 81     | 186                | 186    | 218    | 367                | 376                | 1116   | 1225               | 1549   | 65     | 65                 | 91     |
| Query                    | 100.0              | 100.0  |        |        | 1.00.0 | Ξ.     |        |        | 1.00.0      |         |                    |                  | 93.5   | -      |        | 93.5               |        | 90.3   | 90.3               |        |        |                    |                    |        |                    | 90.3   | 87.1   | 87.1               | 87.1   |
| Score                    | 31                 | 31     | 31     | 31     | 31     | 31     | 31     | 31     | 31          | 31      | 58                 | 53               | 29     | 29     | 29     | 53                 | 29     | 28     | 28                 | 28     | 78     | 78                 | 28                 | 28     | 28                 | 28     | 27     | 27                 | 27     |
| Result<br>No.            | г                  | 7      | æ      | 4      | S      | 9      | 7      | ۵      | σ           | 10      | 11                 | 12               | 13     | 14     | 15     | 16                 | 17     | 18     | 19                 | 50     | 21     | 22                 | 23                 | 24     | 25                 | 56     | 27     | 28                 | 58     |

| Ig kappa chain V r Ig light chain V r acetylcoline recep Ig light chain V r Ig kappa chain V r  | kappa<br>kappa<br>kappa<br>kappa        |
|--|---|
| A38601<br>S59640<br>PC6027<br>PH1077<br>S26343<br>S26344<br>K1HUAU<br>KVMS54<br>PH0092<br>S24288<br>KVMS37   | KVMSC1<br>KVMS43<br>KVMS83<br>KVMS08    |
| 93 2 2 100 1 100 2 2 100 2 2 100 2 2 100 2 100 2 100 8 110 8 1110 2 1110 | 111111111111111111111111111111111111111 |
| 87.1<br>87.1<br>87.1<br>87.1<br>87.1<br>87.1<br>87.1<br>87.1   | 87.1<br>87.1<br>87.1<br>87.1            |
| 7,22<br>7,72<br>7,72<br>7,72<br>7,72<br>7,73<br>7,73<br>7,73   | 27<br>27<br>27<br>27                    |
| 0 1 1 2 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2  | 4 4 4 4<br>5 4 4 3                      |

### ALIGNMENTS

RESULT 1 S25177 Ig kappa chain V region - mouse

C; Species: Mus musculus (house mouse)
C; Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 21-Jan-2000
C; Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 21-Jan-2000
C; Accession: \$25177; 333134
S; Monestier, M.; Fasy, T.M.; Losman, M.J.; Novick, K.E.; Muller, S.
submitted to the EMBL Data Library, July 1992
A; Description: Structure and binding properties of monoclonal antibodies to core hist A; Accession: \$25174

A; Status: preliminary A; Molecule type: mRNA A; Residues: 1-95 <MON>

A;Cross-references: EMBL:X67625; NID:g52146; PIDN:CAA47883.1; PID:g938262 A;Accession: S33134 A;Accession: Sa3134 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-95 <MO2>

A;Residues: 1-95 <MO2>
A;Cross-references: EMBL:X67625; NID:952146; PIDN:CAA47883.1; PID:9938262
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-93/Domain: immunoglobulin homology <IMM>

ö Gaps ; 0 100.0%; Score 31; DB 2; Length 95; 100.0%; Pred. No. 1.8; tive 0; Mismatches 0; Indels Query Match
Best Local Similarity 100.0

1 LASNLES 7 Оp ò

# RESULT

PHIO76

Ig light chain V region (clone 74-c2) - mouse (fragment)
(Species: Mus musculus (house mouse)
(C.Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000
(C.Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000
(C.Date: 30-Sep-1991 #sequence\_revision N.T.; Hill, R.J.; Marion, T.N.

S.Tillian, D.M.; Jou. N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective A;Reference number: PH0971; MUID:92381444

A;Status: nucleic acid sequence not shown A;Molecule type: mRNA A;Residues: 1-102 <TIL>

A; Experimental source: B cell, strain [NZB x NZW]F1 C; Superfamily: immunoglobulin V region; immunoglobulin homology C; Keywords: immunoglobulin F;16-94/Domain: immunoglobulin homology <IMM>

Conservative

Local Similarity

Query Match Best Loc Matches

g

1 LASNLES 7

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Ig kappa chain V region (PC7940) - mouse (tentative sequence)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 31-Mar-2000
C;Accession: C01938; A01938
R;Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A;Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A;Reference number: A93204; MUID:79073152
A;Recession: C01938
A;Molecule type: protein
A;Residues: 1-111 <WEI>C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (C;Complex: An immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin homology < IMM>
F;23-92/Disulfide bonds: #status predicted
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: 125-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C;Accession: D45-20
R;Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Va J.; Virol. 67, 489-496, 1993
A;Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on A;Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on A;Accession: D45722
A;Acc
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C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: Jo-Mar-1997 #sequence_revision 14-Nov-1997 #text_change 07-May-1999
C; Accession: 845715
R; Kim, H. H.; Kato, K.; Yamato, S.; Igarashi, T.; Matsunaga, C.; Ohtsuka, H.; Higuchi, REBS Lett. 346, 246-250, 1994
A; Title: Application of (13)C NMR spectroscopy to paratope mapping for larger antigen A; Reference number: 845714; MUID:94283606
A; Status: nucleic acid sequence not shown; not compared with conceptual translation A; Molecule type: DNA
A; Reperimental source: cell line Ex-3C7
C; Superfamily: Immunoglobulin V region; immunoglobulin homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
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Matches 7; Conservative
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Best Local Similarity 100.
Matches 7; Conservative
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Ig kappa chain V region (PC6684) - mouse (tentative sequence)

C; Species: was musculus (house mouse)

C; Species: was musculus (house mouse)

C; Accession: A01938

R; Weigert, M: Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.

Nature 276, 785-790, 1978

A; Reference number: A93204; MUID: 79073152

A; Recence number: A93204; MUID: 79073152

C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappent disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into lace subunits immunoglobulin V region; immunoglobulin homology

C; Keywords: heterotetramer

F; 16-94/Domain: immunoglobulin homology <IMM>
F; 23-92/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         If Kappa chain V region (PC7175) - mouse (tentative sequence)

C; Species: Mus musculus (house mouse)

C; Species: Mus musculus (house mouse)

C; Accession: B01938, A01938

C; Accession: B01938, A01938

C; Accession: B01938, A01938

A; Itle: Rearrangement of genetic information may produce immunoglobulin diversity.

A; Accession: B01938

A; Accession: B01938

A; Molecule type: protein

A; Molecul
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                                                                                                                                      100.0%; Score 31; DB 2; Length 102; 100.0%; Pred. No. 1.9; 1ve 0; Mismatches 0; Indels
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54 LASNLES 60

1 LASNLES 7

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Best Local Similarity 100.u

54 LASNLES 60

RESULT KVMS40

1 LASNLES 7

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R;Monfardini, C.; Kieber-Emmons, T.; VonFeldt, J.M.; O'Malley, B.; Rosenbaum, H.; God J. Biol. Chem. 270, 6628-6638, 1995
A;Title: Recombinant antibodies in bioactive peptide design.
A;Reference number: A56169; MUID:95204454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: protein
A;Residues: 1-218 <AKA>
C;Comment: This catalytic antibody has peroxidase oxidase. It is directed against a p
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C; Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000
C; Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000
C; Accession: JG5810
R; Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada, Biochem: Biophys, Res. Commun. 240, 566-572, 1997
A; Title: Structural characterization of mouse monoclonal antibody 13-1 against a porp A; Reference number: JC5810; MUID: 980663277
                C;Keywords: heterotetramer; immunoglobulin F;1-20/Domain: signal sequence #status experimental <SIG> F;1-21/JOmain: signal sequence #status experimental <AGI> F;21-131/JOmain: IG Pappa chain precursor V region #status experimental <AMI> F;36-114/Domain: immunoglobulin homology <IMM> F;36-112/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig kappa chain V region (clone 23.2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Oct_1995 #sequence_revision 19-Oct-1995 #text_change 11-Jan-2000
                                                                                                                                                                                                                                                  100.0%; Score 31; DB 1; Length 131; 100.0%; Pred. No. 2.6; Arative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary; not compared with conceptual translation
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Best Local Similarity 100.
Matches 7; Conservative
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Best Local Similarity
7, Conserve
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Best Local Similarity
'-hag 7; Conservē
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A; Residues: 1-210 <MON>
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54 LASNLES 60
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A; Residues: 21-46, 'Q', 48-53,'B', 55-57,'Z', 59-86,'F', 88-131 <MCK>
A; Residues: 21-46,'Q', 48-53,'B', 55-57,'Z', 59-86,'F', 88-131 <MCK>
A; Mote: this sequence has since been revised in reference A93822
B; Motecn, D.J.; Bell, M.; Potter, M.
Proc. Natl. Acad. Sci. U.S.A. 75, 3913-3917, 1978
A; Title: Mechanisms of antibody diversity: multiple genes encode structurally related mc
A; Reference number: A93822; MUID: 79012520
A; Accession: B93822
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C.Comment: The MG3 precursor sequence is shown.
C.Complex: An immunoglobulin heterotetramer submit consists of two identical light (kap hain disulfide bonds. In some cases, such as 1gA and 1gM, the subunits associate into la C.Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Burstein, Y.; Schechter, I.
Biochemistry 17, 2392-2400, 1978
A;Title: Primary structures of N-terminal extra peptide segments linked to the variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Title: Mouse immunoglobulin chains. Pattern of sequence variation among kappa chains
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A; Residues: 21-113, Y', 121-131 <MC3>
A; Residues: 21-113, Y', 121-131 <MC3>
B; Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A; Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A; Reference number: A93204; MUID: 79073152
A; Contents: PC9245; PC4050
                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ig kappa chain precursor V regions (M63, AB22, PC9245, PC4050) - mouse C;Species: Mus musculus (house mouse)
C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 21-Jan-2000 C;Accession: B90412; B93822; C93822; C93204; D93204; PH1078; A01935
                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                           ; Score 31; DB 2; Length 112;
; Pred. No. 2.2;
0; Mismatches 0; Indels
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A; Molecule type: protein
A; Residues: 21-119, 'Y',121-131 <WEI>
A; Accession: D93204
A; Molecule type: protein
A; Residues: 21-119, 'L',121-123,'A',125-129,'L',131 <WE2>
B; Tillman, Dan; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
C; Keywords: heterotetramer; immunoglobulin F;16-94/Domain: immunoglobulin homology <IMM>F;23-92/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       expression of immunoglobulin genes.
A; Reference number: A90412; MUID:78235887
A; Contents: M63
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                                                                                                                                                                 Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 7; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: protein
A; Residues: 1-35 <BUR>
R; McKean, D.; Potter, M.; Hood, L.
Blochemistry 12, 760-771, 1973
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A; Residues: 1-53;69-107 <MC2>
A; Accession: C93822
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A; Molecule type: DNA
A; Residues: 723-741 (LIAG>
A; Residues: 723-741 (LIAG>
A; Cross-references: GB: MA691; NID:g341219; PIDN:AAA48950.1; PID:g531186
B; McCarthy, J.G.; Heywood, S.M.
Nucleic Acids Res. 15, 8069-8085, 1987
A; Title: A long polypyrimidine/polypurine tract induces an altered DNA conformation o
A; Reference number: S01265; MUID:88040428
A; Accession: S01265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A Experimental source: clone Cemb3
R; Moore, L.A.; Arrizubieta, M.J.; Tidyman, W.E.; Herman, L.A.; Bandman, E.,
J. Mol. Biol. 225, 1143-1151, 1992
A; Title: Analysis of the chicken fast myosin heavy chain family. Localization of isof
A; Reference number: $24348; MUID:92309413
A; Rolecule type: mRNA
A; Residues: 1-12,14-741 < WOO2>
A; Residues: 1-12,14-741 < WOO2>
A; Experimental source: clone Cemb3
R; Lagrutta, A.A.; McCarthy, J.G.; Scherczinger, C.A.; Heywood, S.M.
DNA B; 39-50, 1989
A; Title: Identification and developmental expression of a novel embryonic myosin heav
A; Reference number: A30170; MUID:89210285
A; Accession: A30170; MUID:89210285
                                                                                                                                                                                                                                                                           myosin heavy chain, embryonic - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Species: 03-reb-1994 #sequence_revision 03-reb-1994 #text_change 13-Aug-1999
C;Accession: S39082; S24349; A30170; S01265
R;Moore, L.A.; Arrizubieta, M.J.; Tidyman, W.E.; Herman, L.A.; Bandman, E. submitted to the EMBL Data Library, August 1991
A;Description: Analysis of the chicken fast myosin heavy chain family: Localization o A;Reference number: S39081
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A;Residues: 723-741 <MCC>
A;Cross-references: EMBL:X06251; NID:g63600; PIDN:CAA29593.1; PID:g63601
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C;Keywords: actin binding; ATP; coiled coil; muscle
                                                                       Length 230;
                                                                                                             0; Indels
                   F;136,204/Active site: Ser, His #status experimental
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                                                                         Score 29; DB 1;
Pred. No. 15;
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F;125-187/Disulfide bonds: #status experimental
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Pred. No.
                                                                                         Pred. No.
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85.7%;
                                                                         93.5%;
85.7%;
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                                                       Conservative
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nes 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-741 <MOO>
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                                                                                                                                                                                     71 IASNLES 77
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Best Local $
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C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 13-Feb-1998
C;Accession: PSO349
R;Matsuzono, K.; Nagata, S.; Ichikawa, M.; Matsuda, G.
R;Matsuzono, K.; Nagata, S.; Ichikawa, M.; Matsuda, G.
A;Title: Structural Zasshi 66, 311-322, 1991
A;Title: Structural analysis of the chicken myosin heavy chain (comparison M. pectralis A;Reference number: PSO349
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                                                                                                                                                                                                                                                                                                                                                                     Gaps
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0
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A;Note: this peptide is obtained from rod portion
C;Superfamily: myosin heavy chain; myosin motor domain homology
C;Keywords: ATP
                                                                                                                                                                                                                                                                                                                             Score 29; DB 2; Length 94; Pred. No. 5.6;
                                                                                                                                                                                                                                                                                                                                                                     0; Indels
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                                                                                                                                                                                                                                                                                                                               93.5%;
85.7%;
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Best Local Similarity
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myosin heavy chain, neonatal [similarity] - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Dacte: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 20-Jun-2000
C;Accession: S39083; S24350; A26821
R;Moore, L.A.; Arrizubieta, M.J.; Tidyman, W.E.; Herman, L.A.; Bandman, E.
                                                                 Gaps
                                                                 ö
Length 741;
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A Molecule type: mRNA
A; Residues: 1-936 <MOOL)
A; Residues: 1-936 <MOOL)
A; Cross. teferences: EMBL: M74087
B; Moore, L.A.; Arrizubleta, M.J.; Tidyman, W.E.; Herman, L.A.; Bandman, E.
J. Mol. Biol. 225, 1143-1151, 1992
J. Mol. Biol. 225, 1143-1151, 1992
A; Title: Analysis of the chicken fast myosin heavy chain family. Localization of isoform A; Reference number: S24348; MUID: 92309413
A; Accession: S24350
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C.Species: Gallus gallus (chicken)
C.Species: Gallus gallus (chicken)
C.Oate: 03-Feb-1994 #sequence_revision 06-Sep-1996 #text_change 13-Feb-1998
C.Accession: S24348
R.Moore, L.A.; Arrizubleta, M.J.; Tidyman, W.E.; Herman, L.A.; Bandman, E.
A.Title: Analysis of the chicken fast myosin heavy chain family. Localization of isoform A; Reference number: S24348
A.Accession: S24348
A.Accession: S24348
A.Molecule type: mRNA
A.Residues: 1-955 cMOD
A.Gross-references: EMBL:M74085
C.Superfamily: myosin heavy chain; myosin motor domain homology
C.Keywords: ATP; coiled coil; muscle contraction; skeletal muscle; thick filament
submitted to the EMBL Data Library, August 1991
A; Description: Analysis of the chicken fast myosin heavy chain family: Localization of
A; Reference number: $39081
A; Accession: $39083
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A; Residues: 3-466, Q',468-641, 'R',643-936 <MOO2>
A; Cross: references: EMBL:M74087
E; Moriarity, D.M.; Barringer, K.J.; Dodgson, J.B.; Richter, H.E.; Young, R.B.
DNA 6, 91-99, 1987
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A;Residues: 'F',856-936 <MOR>
A;Crossreferences: GB:M16557; NID:g212371; PIDN:AAA48970.1; PID:g212372
C;Genetics:
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C'Keywords: actin binding; ATP; coiled coil; muscle; skeletal muscle
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85.7%; Pred. No. 72;
Live 1; Mismatches 0; Indels
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Matches 6; Conservative
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232 LASNMES 238
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Search completed: June 28, 2001, 15:58:46 Job time: 374 sec

1111:11 250 LASNMES 256

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

June 28, 2001, 15:54:39 ; Search time 105.36 Seconds (without alignments) 2.276 Million cell updates/sec Run on:

US-09-724-406-30 31 1 LASNLES 7 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

93435 Total number of hits satisfying chosen parameters:

93435 seqs, 34255486 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_39:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| SUMMAKIES  |        | Describtion | OUSE P01662 mus musculu | P01663 mus | P01670 mus | P01671 mus | P01672 mus | P01661 mus | 099174 fusa | USSO PO0590 fusarium | HICK P13538 gallus ga | HICK P02565 gallus | Q9uyd4 pyroco | 058211     | 017963     |            | P47551     | P40438     |            |            | P01674 1   | P01668 mus | P01660 mus | P01664 mus | OUSE P01665 mus musculu |            | OUSE P01667 mus musculu | NOUSE P01669 mus musculu | 09zdq9     | P40339     |            | P43556     | MODE ACCIDE |
|------------|--------|-------------|-------------------------|------------|------------|------------|------------|------------|-------------|----------------------|-----------------------|--------------------|---------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|-------------------------|------------|-------------------------|--------------------------|------------|------------|------------|------------|-------------|
| SOS<br>SOS | £      | - ;         | KV3J_MOUS               | KV3K_MOUSE | KV3R_MOUSE | KV3S_MOUSE | KV3T_MOUSE | KV3I_MOUSE | CUTI_FUSSC  | CUTI_FUSSO           | MYSS_C                | MYSE_CHICK         | NADM_P        | NADM_PYRHO | YKY4_CAEEL | YN94_YEAST | X309_MYCGE | YIR3_YEAST | YJW2_YEAST | KV1B_HUMAN | KV3V_MOUSE | KV3P_MOUSE | KV3H_MOUSE | KV3L_MOUSE | KV3M_MOUSE              | KV3N_MOUSE | KV30_MOUSE              | KV3Q_MOUSE               | Y359_RICPR | RFC4_YEAST | YIEO_HAEIN | YFE7_YEAST | MUDAN OCCA  |
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|            | Longth |             | 111                     | 111        | 111        | 111        | 111        | 131        | 230         | 230                  | 1938                  | 1940               | 186           | 186        | 376        | 1116       | 1225       | 1549       | 1549       | 108        | 108        | 110        | 111        | 111        | 111                     | 111        | 111                     | 111                      | 155        | 323        | 463        | 714        | 202         |
| ФP         | Query  |             | 100.0                   | 100.0      | 100.0      | 100.0      | 100.0      | 100.0      | æ,          | ë.                   | 93.5                  | r)                 | 0             | 90.3       | 0          | 0          | 90.3       | 90.3       | 90.3       | 87.1       | 87.1       | 87.1       | 87.1       | 87.1       | 87.1                    | 87.1       | 87.1                    |                          | 87.1       | 87.1       | 87.1       | 87.1       |             |
|            | grove  |             | 31                      | 31         | 31         | 31         | 31         | 31         | 29          | 29                   | 29                    | 53                 | 28            | 28         | 28         | 28         | 28         | 28         | 87         | 27         | 27         | 27         | 27         | 27         | 27                      | 27         | 27                      | 27                       | 27         | 27         | 27         | 27         |             |
|            | Result |             | П                       | ~          | m          | 4          | 2          | 9          | 7           | 8                    | on (                  | 10                 | 11            | 12         | T .        | 41         | 15         | 16         | 7,         | 81         | 19         | 50         | 21         | 22         | 23                      | 24         | 25                      | 26                       | 27         | 28         | 53         | 30         | -           |

PRT; 111 AA.

STANDARD;

RESULT 2 KV3K\_MOUSE ID KV3K\_MOUSE AC P01663;

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| mus musculu haemophilus synechocyst dictyosteli dictyosteli drosophila homo sapien saccharomyc canis famil schizosacch bacteriopha bacteriopha caenorhabdi  | eostomi; nae; Mus. structurally iobulin in. 1. 2. 2.  | Gaps 0:  |
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| P01658 m<br>P71398 h<br>P73555 s;<br>P73509 d<br>P73609 d<br>P7 | ebrata; Euteleostomi; Muridae; Murinae; Mus genes encode structur 978). J., Hood L.E.; Oduce immunoglobulin UENCES ARE IDENTICALDETERMINING 1DETERMINING 3.   | Length 111;<br>Indels 0;                                 |
| KV3F_MOUSE LSG4_HAEIN Y875_SYNY3 KAPC_DICDI MABN_DROME MYSS_HUMAN RS18_YEAST CSF3_CANFA YDA4_SCHPO VIN3_BPT4 YQCC_CAEEL ALGNMENTS   | T; 111 AA.  ation update 22/PC 9245.  aniata; Vert iurognathi;  iurognathi;  saj13-3917(1 saj13-3917(1 cons.; schilling ation may pr D PC9241 SEG D PC9241 SEG D PC9241 SEG WEWORK 1. PLEMENTARITY WEWORK 2. PLEMENTARITY WEWORK 3. STATILARITY SIMILARITY SIMILARITY.  | Score 31; DB 1; Le<br>Pred. No. 0.78;<br>; Mismatches 0; |
| 232<br>2532<br>2532<br>2532<br>11465<br>11465<br>1191<br>1191<br>1193<br>1193<br>1194<br>1197<br>1197<br>1197<br>1197<br>1197<br>1197<br>1197   | BP C c . 1  | 100.0%;<br>100.0%;<br>ive 0                              |
| 888833.99<br>8833.99<br>8800.99<br>900.66<br>900.66<br>900.66<br>900.66<br>900.66<br>900.66   | BE STANDARD;  B6 (Rel. 01, Car  B6 (Rel. 01, La  199 (Rel. 38, La  CHAIN V-III REG  LULS (Mcuse).  Rutheria; Rode  CABEC 22.  19012520; Pubmed  J., Bell M., Po  J.,   | 100<br>Similarity 100<br>7; Conservative                 |
| 20220200000000000000000000000000000000  | LT 1  MOUSE STANDARD;  P01662;  21-JUL-1986 (Rel. 01, Car 21-JUL-1986 (Rel. 01, Lel 15-JUL-1989 (Rel. 38, Lel 15-JUL-1999 (Rel. 38, Lel 16 KAPPA CHAHN V-III REG MUS musculus (Mouse).  Eukaryota; Metazoa; Chor Musmila; Eutheria; Rode NCBL TaxID-10090;  SEQUENCE (ABPC 22).  WECHANDARD OF CASION (1)  Eukaryota; Metazoa; Chor MUSMILNE-79012520; PubMed NCKean D.J., Bell M., Po "Mechanisms of antibody related mouse kappa vari Proc. Natl. Acac. 261. 0  SEQUENCE (PC 9245).  MEDLINE-79073152; PubMed Weigert M., Gatmaitan L. "Mesarrangement of geneti diversity."; S-790(1978)  "Nature 276:185-790(1978)  "Nature 276:185-790(1978)  "Nature 276:185-790(1978)  "Inmunoglobulin v region. DOMAIN 1 24 38 DOMAIN 10 21 DOMAIN 10 21 DOMAIN 11 111 SEQUENCE 111 AA; 1204  | Simi<br>7;   |
| 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8   | RESULT 1  KV3J_MOUSE  DT 21-JUI  DT 21-JUI  DT 15-JUI  DT 15-JUI  DT 15-JUI  DE IG KAP  OS MAINTAIL  OC MAINTAIL  OC MAINTAIL  RA MCKEAIN  RA MCKEAIN | Query Match<br>Best Local<br>Matches                     |

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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae, Murinae; Mus
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Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
"Rearrangement of genetic information may produce immunoglobulin
                                                                                                                MEDLINE-79073152; PubMed-103003; Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.; "Rearrangement of genetic information may produce immunoglobulin
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COMPLEMENTARITY - DETERMINING 3.
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-III REGION PC 4050.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1G KAPPA CHAIN V-III REGION PC 6684.
Mus musculus (Mouse).
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PIR: A01938; KVMSS4.
InterPro; IPR003006; -.
Péan; PF00047; 19; 1.
Immunoglobulin V region.
                                                                                                                                                    diversity.";
Nature 276:785-790(1978).
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InterPro; IPR003006; -.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                       Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.; Rearrangement of genetic information may produce immunoglobulin
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100.0%; Score 31; DB 1; Length 111; llarity 100.0%; Pred. No. 0.78; Conservative 0; Mismatches 0; Indels
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG RAPPA CHRIN V-III REGION PC 7940.
                                                                                                                                                                       21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15 JUL-1999 (Rel. 38, Last annotation update)
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0; Mismatches
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MEDLINE=79073152; PubMed=103003;
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Matches 7; Conservative
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InterPro; IPR003006; -.
Pfam; PF00047; ig; 1.
Immunoglobulin V region.
 Query Match
Best Local Similarity
Matches 7; Conserv
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                                                     1 LASNLES 7
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P01671;
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P01672;
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KV3S_MOUSE
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Blochemistry 17:2392-2400(1978).
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MEDLINE-73140225; PubMed-4691517;

MCRean D.J., Potter M., Hood L.E.;

"Mouse immunoglobulin chains. Pattern of sequence variation among kappa chains with limited sequence differences.";

Blochemistry 12:760-771(1973).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                      FRAMEWORK 2. COMPLEMENTARITY-DETERMINING 2.
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Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
PIR, A01935; KWANSMG.
Interpro: IPRO3006; -.
Pfam; PF00047; 19; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-III REGION MOPC 63 PRECURSOR
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                                                                                                                                                                                                                                                                          12038 MW;
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Nature 276:785-790(1978)
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                PIR; C01938; KVMS40.
InterPro; IPR003006; -.
                                                     Pfam; PF00047; 1g; 1.
Immunoglobulin V region.
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111 AA;
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Best Local Similarity
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KV31_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Crowhurst R.N., Binnie S.J., Bowen J.K., Hawthorne B.T., Plummer K.M., Rees-George J., Rikkerink B.H., Templeton M.D.; Effect of disruption of a cutinase gene (cutA) on virulence and tissue specificity of Fusarium solani f. sp. cucurbitae race 2 toward Cucurbita maxime and C. moschata.
                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOI. Plant Microbe Interact. 10:355-368(1997).

-!- FUNCTION: ALLOWS PATHOGENIC FUNGI TO PENETRATE THROUGH THE
CUTICULAR BARRIER INTO THE HOST PLANT DURING THE INITIAL STAGE
OF THE FUNNAL INFECTION (BY SIMILARITY).

-!- CATALYTIC ACTIVITY: HYDROLYSIS OF CUTIN, A POLYESTER THAT
FORMS THE STRUCTURE OF PLANT CUTICLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: SECRETED.
PTM: THE 2 DISULFIDE BONDS PLAY A CRITICAL ROLE IN HOLDING THE
CATALYTIC RESIDUES IN JUXTA-POSITION; REDUCTION OF THE DISULFII
BRIDGES RESULTS IN THE COMPLETE INACTIVATION OF THE ENZYME (BY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fusarium solani (subsp. cucurbitae) (Nectria ipomoeae).
Eukaryota; Fungl; Ascomycota; Pealzomycotina; Sordariomycetes;
Hypocreales; Nectriaceae; Nectria.
NCBL_TaxID=57162;
                                                                                                                                            100.0%; Score 31; DB 1; Length 131; 100.0%; Pred. No. 0.94;
                                                                                                                                                                                           0; Indels
                                                                        D212EC9F08DC880A CRC64;
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SIGNAL 1 16 BY SIMILARITY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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     FRAMEWORK 4
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MEDLINE=97254998; Pubmed=9100380;
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                                               131
14291 MW;
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                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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187
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Best Local Similarity
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131 AA;
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"Structure of the cutinase gene and detection of promoter activity in the 5'-flanking region by fungal transformation."; 
J. Bacteriol, 171:1942-1951(1989).
                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-92220194; PubMed-1560844; Matthyssens G., Cambillau C.; Martinez C., de Geus P., Lauwereys M., Matthyssens G., Cambillau C.; Fusarium solani cutinase is a lipolytic enzyme with a catalytic serine accessible to solvent.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Martinez C., Nicolas A., van Tilbeurgh H., Egloff M.-P., Cudrey C., Verger R., Cambillau C.; "Cutinase, a lipolytic enzyme with a preformed oxyanion hole."; Biochemistry 33:83-89(1994).
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Hilbers C.W.;
"IH, 13C, and 15N resonance assignments of Fusarium solani pisi cutinase and preliminary features of the structure in solution.";
Protein Sci. 6:2375-2384(1997)
-i- FUNCTION: ALLOWS PATHOGENIC FUNCI TO PENETRATE THROUGH THE CUTICULAR BARRIER INTO THE HOST PLANT DURING THE INITIAL STAGE
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Longhi S., Czjack M., Lamazin V., Nicolas A., Cambillau C.;
"Atomic resolution (1.0 A) crystal structure of Fusarium solani
cutinase: stereochemical analysis.";
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                                                                                                                                                                                                                                                                                                                                                                                                    Fusarium solani (subsp. pisi) (Nectria haematococca).
Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Fusarium.
NCBI_TaxID=109625;
                                                   Score 29, DB 1; Length 230;
Pred. No. 5.7;
1; Mismatches 0; Indels
230 AA; 23902 MW; 05FB3C33326405AA CRC64;
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                                                                                                                                                                                                                                                                                                      21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                  230 AA
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Submitted (MAR-1997) to the PDB data bank.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
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                                                     Query Match 93.5%;
Best Local Similarity 85.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 356:615-618(1992).
                                                                                                                                                                                                                                                                    STANDARD;
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                                                                                                                                                       :||||||
71 IASNLES 77
                                                                                                                               1 LASNLES 7
                                                                                                                                                                                                                                                                CUTI_FUSSO
P00590;
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SEQUENCE
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ID CUTI_F
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            Hydrolase; Serine esterase; Glycoprotein; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLUCURONIC ACID.
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                                                                                                                                                                                                                                                                                                                                                                         M29759; AAA33335.1; -.
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OF THE FUNGAL INFECTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       230
32
194
187
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PIR; A32836, A32836.
PDB; ICUS; 31-JUL-94.
PDB; 2CUT; 31-AUG-94.
PDB; ICUA; 11-JUL-96.
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1FFD;
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"The primary structure of skeletal muscle myosin heavy chain: IV.
Sequence of the rod, and the complete 1,938-residue sequence of the
                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Malta T., Miyanishi T., Matsuzono K., Tanioka Y., Matsuda G.;
"The primary structure of skeletal muscle myosin heavy chain: III.
Sequence of the 22 kDa fragment and the alignment of the 23 kDa,
kDa, and 22 kDa fragments.".
J. Biochem. 110:68-74(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Komine Y., Maita T., Matsuda G.;
"The primary structure of skeletal muscle myosin heavy chain: II.
Sequence of the 50 kDa fragment of subfragment-1.";
J. Blochem. 110:60-67(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Pectoralis muscle;
MEDLINE-22041767; PubMed-1930027;
Hayashida M., Maita T., Matsuda G.;
"The primary structure of skeletal muscle myosin heavy chain: I.
Sequence of the amino-terminal 23 kDa fragment.";
J. Blochem. 110:54-59(1991).
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                                                                                                                      Score 29; DB 1; Length 230;
Pred. No. 5.7;
1; Mismatches 0; Indels
                                             R -> A (IN REF. 2).
R -> A (IN REF. 2).
7253ACAA657ADIAB CRC64;
                                                                                                                                                                                                                                                                                                             01-JAN-1990 (Rel. 13, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
MACSIN HEAVY CHAIN, SKELETAL MUSCLE, ADULT.
Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Pectoralis muscle;
MEDLINE-92041768; PubMed-1939028;
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MEDLINE-92041769; PubMed-1939029;
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MEDLINE-92041770; Pubmed-1939030;
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                                             48 R
94 R
23982 MW;
                                                                                                                      93.5%;
85.7%;
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                                                                                                                                                    6; Conservative
                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 206-636.
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                                                                       230 AA;
                                                                                                                     Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-205.
                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID-9031;
 136
191
204
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94
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71 IASNLES 77
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P13538;
ACT_SITE
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CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C -1- FUNCTION: MUSCLE COMTRACTION. MYOSIN IS A PROTEIN THAT BINDS TO
F-ACTIN AND HAS ATPASE ACTIVITY THAT IS ACTIVATED BY F-ACTIN.
C -1- SUBMUT: MUSCLE MYOSIN IS A HEXAMENC PROTEIN THAT CONSISTS OF 2
HEAVY CHAIN SUBMUTS (MAC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
AND 2 REGULATORY LICHT CHAIN SUBMUTS (MLC-2).
C -1- SUBCELLULAR LOCATION: THICK FILAMENTS OF THE MYOFIBRILS.
C -1- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING
C CYCLES OF A 28-RESTOUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
C CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
C -1- PTM: TWO CYSTERINE RESIDIES IN THE SI DOMAIN ARE SELECTIVELY
ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.
C -1- MISCELLANGOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT
MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE
C SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (SI) AND 1 ROD-SHAPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBFRAGMENT (S2).
SIMILARITY: THE PERIODICITIES OF HYDROPHOBIC AND CHARGED RESIDUES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Three-dimensional structure of myosin subfragment-1: a molecular
                                                                                                                                                     'Amino-acid sequence of the short subfragment-2 in adult chicken
                Complete amino acid sequence of subfragment-2 in adult chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WHICH DICTATE THE ALPHA-HELICAL COILED-COIL STRUCTURE ARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Genomic clones encoding chicken myosin heavy-chain genes."; DNA 6:91-99(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 1-843.
MADLINE-33333624; Pubmed-8136857;
MASYMENT I., Rypniewski W.R., Schmidt-Base K., Smith R.,
Tomchick D.R., Benning M.M., Winkelmann D.A., Wesenberg G.,
                                                                                                                                                                                                                                                                   Watanabe B.;
"Amino-acid sequence of the hinge region in chicken myosin
                                                                                                                                                                                                                                                                                                                                                                                                              Moriarity D.M., Barringer K.J., Dodgson J.B., Richter H.E.
Young R.B.;
                                  skeletal muscle myosin.";
Biol. Chem. Hoppe-Seyler 370:1027-1034(1989)
                                                                                                                                                                                         Biol. Chem. Hoppe-Seyler 370:549-558(1989)
                                                                                                                                                                                                                                                                                                                                Biol. Chem. Hoppe-Seyler 370:55-61(1989)
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1857-1938 FROM N.A. MEDLINE-87217964; PubMed=3034534;
                                                                                                              MEDLINE-89374803; PubMed=2775482;
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Pfam; PF01576; Myosin_tail; 1.
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PIR; AZ6821; AZ6821.
PIR; S02082; S02082.
PIR; S04501; S04501.
PIR; S05515; S05515.
InterPro; IPR000048; ...
InterPro; IPR0005928; ...
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Science 261:50-58(1993).
                                                                                                                                                                     skeletal muscle myosin.
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                                                                                         SEQUENCE OF 852-1108
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Watanabe B.;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-87194881; PubMed=3571266;
Molina M.I., Kropp K.E., Gulick J., Robbins J.;
"The sequence of an embryonic myosin heavy chain gene and isolation
                             Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding; ATP-binding; Methylation; Alkylation; Phosphorylation; Acetylation; Heptad repeat pattern; Multigene family; 3D-structure.

GLOBULAR HEAD (S1)
                                                                                                                                                                                                                                                                                                                        ;
                                                                                  RODLIKE TAIL (S2 AND LMM DOMAINS).
ALPHA-HELICAL TAILPIECE (S2).
                                                                                                                                                                                                                                                                                                  93.5%; Score 29; DB 1; Length 1938;
85.7%; Pred. No. 63;
                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                  ALKYLATION (SH-1).
ALKYLATION (SH-2).
C -> Q (IN REF. 6 AND 7).
I -> V (IN REF. 9).
IHG -> FH (IN REF. 9).
                                                                                                                                                                                                                                                                     C7A42230FEBD2425 CRC64;
                                                                                                                LIGHT MEROMYOSIN (LMM).
COILED COIL (POTENTIAL)
ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUL-1986 (Rel. 01, Created)
1-EBA-1996 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
MYOSIN HEAVY CHAIN, FAST SKELETAL MUSCLE, EMBRYONIC.
                                                                                                                                                                           METHYLATION (MONO-).
METHYLATION (TRI-).
METHYLATION (TRI-).
METHYLATION (MONO-).
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                                                                                                                                             ACTIN-BINDING.
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                                                                                                                                                                   ACETYLATION.
                                                                          HINGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biol. Chem. 262:6478-6488(1987)
                                                                                                                                                                                                                                                                      222972 MW;
Pfam; PF00063; myosin_head; 1.
PRINTS; PR00193; MYOSINHEAVY.
PROSITE; PS50096; IQ; 1.
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P02565;
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MYSE_CHICK
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01-OCT-2000 (Rel. 40, Last annotation update)
NICOINAMDE-NUCLEOTIDE ADBNYLXITERANSFERSE (EC 2.7.7.1) (NAD(+)
PYROPHORYLASE) (NAD(+) DIPHOSPHORYLASE) (NAN ADENYLXITERANSFERASE).
DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMEDSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COLLED COLLS.

PHY: TWO CYSTEINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY MISCELLANGOUS: EACH MOSIN (HAN) CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LMM) AND I HEAVY MEROMYOSIN (HMM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (SI) AND I ROD-SHAPED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATP-binding; Methylation; Alkylation; Multigene family.

DOMAIN 1 843 GADBULAR HEAD (S1).

BODAIRE TAIL (S2 AND LAW DOMAINS).

DOMAIN 844 1940 COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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METHYLATION (TRI-) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93.5%; Score 29; DB 1; Length 1940;
85.7%; Pred. No. 64;
                                                                                                                                                                                                                                                  SUBFRAGMENT (S2). SIMILARITY: BELONGS TO THE MYOSIN HEAVY CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -> A (IN REF. 2).
AA -> GRT (IN REF. 2).
C34833D75B04DFF2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALKYLATION (SH-1). ALKYLATION (SH-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       186 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACTIN-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ERA -> GRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G - D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            222816 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2000 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00612; IQ; 1.
Pfam; PF01576; Myosin_tail; 1.
Pfam; PF00063; myosin_head; 1.
PRINTS; PR00193; MYOSINHEAVY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; V00430; CAA23712.1; -. EMBL; J02714; AAA48972.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR, A02990, A02990.
PIR, A29320, A39320.
HSSP, P13538, 2MYS.
InterPro, IPR000048; -.
InterPro, IPR001609; -.
InterPro, IPR002928; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50096; IQ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1940
1940
186
682
776
130
700
710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ¥¥;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1236 LASNMES 1242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pyrococcus abyssi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1547
1913
1940
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NADM_PYRAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9UYD4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PAB1318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NADM_PYRAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
                  SO TITITITITI THE TITITITI SO TO THE SOURCE COULD BE SOURCE CO
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SEQUENCE FROM N.A.

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C14B1.4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Definition of the state of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0CT-2000 (Rel. 40, Created)
01-0CT-2000 (Rel. 40, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
01-0CT-2000 (Rel. 40, Last annotation update)
NICOTINAMIDE-NUCLEOTIDE ADENTLYTRANSFERASE (EC 2.7.7.1) (NAD(+)
PYROPHOSPHORYLASE) (NAD(+) DIPHOSPHORYLASE).
                                            Pyrococcus abyssi genome sequence: insights into archaeal chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
                                                                                                                                                                  -i- SUBCELLUTAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- PATHWAY: NAD BIOSYNTHESIS.
-1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
-1- SIMILARITY: BELONGS TO THE ARCHAEAL NWN ADENYLYLTRANSFERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA RES. 5:55-76(1998).
-1- CATALYTIC ACTIVITY: ATP + NICOTINAMIDE RIBONUCLEOTIDE =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90.3%; Score 28; DB 1; Length 186; 85.7%; Pred. No. 7.9; 1ve 1; Mismatches 0; Indels
                                                            structure and evolution.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ATP + NICOTINAMIDE RIBONUCLEOTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam. PF01467; Cytidylyltransf; 1.
Transferase; Nucleotidyltransferase; NAD.
SEQUENCE 186 AA; 21417 MW; E8230B688481386E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        186 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                          DIPHOSPHATE + NAD(+)
                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AJ248288; CAB50478.1; -. InterPro; IPR001994; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DIPHOSPHATE + NAD(+)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pyrococcus horikoshii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=53953;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             166 LATNLES 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 LASNLES 7
STRAIN-ORSAY;
                                                                                                                                                                                                                 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NADM_PYRHO
                        Heilig R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     058211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NADM_PYRHO
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
HYPOTHETICAL 40.4 KDA TRP-ASP REPEATS CONTAINING PROTEIN C14B1.4 IN
                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                    90.3%; Score 28; DB 1; Length 186; 85.7%; Pred. No. 7.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90.3%; Score 28; DB 1; Length 376; 85.7%; Pred. No. 18; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
-!- SIMILARITY: STRONG, TO KO4G11.4 AND ZC302.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                      InterPro; IPR001994; --
Pfam; PF01467; Cytidylytransf; 1.
Transferase; Nucleotidyltransferase; Nab.
SEQUENCE 186 Aa; 21392 MW; 1CE5A40C884ADB34 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3204DC36FE58FC19 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              376 AA.
                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                  EMBL; AP000002; BAA29550.1;.-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40393 MW;
                                                                                                                                                                                                                                                                               6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Lase 6; Conserva
                                                                                                                                                                                                                                                    Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               341
376 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                               ||:||||
|166 LATNLES 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHROMOSOME III.
                                                                                                                                                                                                                                                                                                                      1 LASNLES 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YKY4_CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Harris B.;
                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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Search completed: June 28, 2001, 15:54:39 Job time: 127 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
                                                                                                                                                                                                                                                                                                                                                                               TIGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                         LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
δŏ
                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its web yn ono-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                      Duesterhoeft A., Floeth M., Fritz C., Heuss-Neitzel D.,
Hilbert H., Moestl D.;
Submitted (MAY-1994) to the EMBL/GenBank/DDBJ databases.
-- SIMILARITY: BELONGS TO THE PEPI FAMILY OF MEMBRANE GLYCOPROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                          01-ocT-1996 (Rel. 34, Created)
1-ocT-1996 (Rel. 34, Last sequence update)
01-ocT-1996 (Rel. 34, Last annotation update)
pUTATIVE 125.2 KDA MEMBRANE GLYCOPROTEIN IN BIO3-HXI17 INTERGENIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED (GLCNAC. .) (POTENTIAL).
W. C0361878FE4DAB90 CRC64;
                                                                                                                                                                                Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90.3%; Score 28; DB 1; Length 1116;
85.7%; Pred. No. 60;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transmembrane; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1996 (Rel. 33, Last sequence update) 01-NOV-1997 (Rel. 35, Last annotation update) HYPOTHETICAL LIPOPROTEIN MG309 PRECURSOR. MG309,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1225 AA.
                                                                                    PRT; 1116 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35 35 N-LII
336 336 N-LII
553 553 N-LII
846 846 N-LII
985 985 N-LII
1116 AA; 125199 MW; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Y309_MYCGE STANDARD; F
P47551; Q49317;
01-FEB-1996 (Rel. 33, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycoplasmataceae; Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; Z71680; CAA96347.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity 85./۰
اجماع 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=ATCC 33530 / G-37;
                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             957
335
336
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985
                                                                                                                                                                                                                                                                                                                                                                                                                               SGD; S0005348; YNR065C
                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002860; -. Pfam; PF02012; BNR; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycoplasma genitalium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein;
                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                534 LATNLES 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=2097;
              11111:1
272 LASNLDS 278
                                                                                                                                                                       YNR065C OR N3539
                                                                                                                                                                                                                     NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 LASNLES 7
1 LASNLES 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical
                                                                                   YN94_YEAST
P53751;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
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                                                            RESULT 14
YN94_YEAST
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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MEDLINE=96026346; PubMed=756993; Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A., Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A., Frleischmann R.D., Bult C.J., Kerlavage A.R., Suuton G., Kellay J.M., Fritchmann J.L., Weidman J.F., Small R.V., Sandusky M., Fuhrmann J.L., Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M., Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S., Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.; "The minimal gene complement of Mycoplasma genitalium.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-ATCC 33530 / G-37;
MEDLINE-9407520; PubMed-8253680;
Peterson S.N., Hu P.-C., Bott K.F., Hutchison C.A. III;
"A survey of the Mycoplasma genitalium genome by using random
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequencing.";
J. Bacteriol. 175.7918-7930(1993).
-!- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A LIPID ANCHOR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-ACYL DIGLYCERIDE (POTENTIAL).
L -> V (IN REF. 2).
W; C3E4BF5B4319B6E8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: BELONGS TO THE MG307 / MG309 / MG338 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL LIPOPROTEIN MG309.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90.3%; Score 28; DB 1; Length 1225; 85.7%; Pred. No. 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYPOTHE; PS00013; PROKAR_LIPOPROTEIN; 1.
Hypothetical protein; Lipoprotein; Membrane; Signal.
SIGNAL 1 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1185 1185 L -
1225 AA; 138375 MW;
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1138-1224 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U39711; AAC71531.1; -. EMBL; U02200; AAD12488.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28
1185
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           286 LASNLQS 292
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 us-09-724-406-30.rspt

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

June 28, 2001, 16:08:27 ; Search time 411.58 Seconds (without alignments) 2.250 Million cell updates/sec Run on:

US-09-724-406-30 Title:

1 LASNLES 7 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

425026 seqs, 132305027 residues Searched:

425026 Total number of hits satisfying chosen parameters:

Minimum DB seq length; 0 Maximum DB seq length; 2000000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 08

SPTREMBL\_16:\* Database :

sp\_archea:\* sp\_bacteria:\*

sp\_invertebrate:\* sp\_organelle:\* sp\_mammal:\* sp\_fungi:\* sp\_human:\* sp\_mhc:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp\_unclassified:\*
sp\_vertebrate:\*

sp\_virus:\*

sp\_rodent:\*

12::::

sp\_plant:\*

sp\_phage:\*

#### CITORADIE

| RIES      | ٠      | Description     | O91i76 arabidonsis | O9vhd5 rana catesh | 09v706 drosophila | 013228 031115 | Ogotv2 gallus gall | Ogdana calles | Ogdam5 aallus aall | 022481 caenorhahdi | 09x5a4 trenonema d | 082521 ransicim ch | Ogyhd7 rana catash | Ogvhda rana catesh | O9fhh2 arabidonsis | 095054 trichomonas |        |        | _      | 015785 homo canton |        |
|-----------|--------|-----------------|--------------------|--------------------|-------------------|---------------|--------------------|---------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|--------|--------|--------------------|--------|
| SUMMARIES |        | er :            | 961160             | Q9YHD5             | 907760            | 013228        | O9PTY2             | 09DGM4        | O9DGM5             | 022481             | 09X5A4             | 082521             | 09YHD7             | 09YHD8             | 09 ЕНН 2           | 095054             | 095055 | 056271 | 09U2Y4 | 015785             | 09NTZ3 |
|           |        | BB              | 10                 | 13                 | Ŋ                 | 13            | 13                 | 13            | 13                 | S                  | ~                  | 10                 | 13                 | 13                 | 10                 | S                  | 'n     | 7      | ഗ      | 4                  | 4      |
|           |        | Match Length DB | 443                | 826                | 856               | 1939          | 1939               | 1941          | 1944               | 367                | 393                | 459                | 708                | 879                | 990                | 125                | 125    | 190    | 204    | 309                | 309    |
| đ         | Query  | Match           | 100.0              | 100.0              | 93.5              | 93,5          | 93.5               | 93.5          | 93.5               | 90.3               | 90.3               | 90.3               | 90.3               | 90.3               | 90.3               | 87.1               | 87.1   | 87.1   | 87.1   | 87.1               | 87.1   |
|           |        | Score           | 31                 | 31                 | 29                | 29            | 29                 | 29            | 29                 | 28                 | 28                 | 28                 | 28                 | 28                 | 28                 | 27                 | 27     | 27     | 27     | 27                 | 27     |
|           | Result | SO.             | 1                  | 7                  | 3                 | 4             | S                  | 9             | 7                  | <b>&amp;</b>       | O                  | 10                 | 11                 | 12                 | 13                 | 14                 | 15     | 16     | 17     | 18                 | 19     |

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Gaps

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Indels

Ouery Match 100.0%; Score 31; DB 10; Length 443; Best Local Similarity 100.0%; Pred. No. 19; Matches 7; Conservative 0; Mismatches 0; Indels 0

| Q9saf7 arabidopsis Q9gy2 ureaplasma Q9sr09 arabidopsis Q91sx2 arabidopsis Q9lsx2 arabidopsis Q9kln8 vibrio chol O42938 schizosacch O54807 mus musculu Q9pun2 xenopus lae O75162 homo sapien Q9fnf5 arabidopsis Q27095 trichomonas Q277095 trichomonas Q277095 trichomonas |   |
|---|---|
| 10 09SAF7<br>2 09PQY2<br>10 09SR09<br>10 09LSX2<br>09LSX2<br>042938<br>11 054807<br>11 054807<br>10 09FNF5<br>5 027795<br>5 025757  | 1 058242<br>2 056707<br>2 055707<br>2 052004<br>2 051353<br>2 091353<br>10 092W18<br>10 092W18<br>10 092W18<br>3 090705<br>5 090705 |
|   | 123<br>136<br>158<br>190<br>207<br>268<br>268<br>269<br>271<br>282<br>355   |
| 87.1<br>87.1<br>87.1<br>87.1<br>87.1<br>87.1<br>87.1<br>87.1  |   |
| 222222222222  | 66666666666666666666666666666666666666  |
| 01222222222222222222222222222222222222  | E E E E E E E E E E E E E E E E E E E   |

## ALIGNMENTS

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Nakamura Y.;
"Structural analysis of Arabidopsis thaliana chromosome 3. II.
Sequence features of the regions of 4,251,695 bp covered by ninety Pl,
                                                                                                                          Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                   STRAIN-COLOMBIA;
Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 443 AA; 49318 MW; 1E2D37B3F9066F4C CRC64;
                                                            01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
SIMILARITY TO ELICITOR-INDUCIBLE RECEPTOR EIR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00572; GLYCOSYL_HYDROL_F1_1; UNKNOWN_1.
SMART; SM00370; LRR; 1.
                                  443 AA.
                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                         TAC and BAC clones.";
DNA Res. 7:217-221(2000).
EMBL, AP001313; BAB03087.1; ..
InterPro; IPR001560; ..
InterPro; IPR001511; ..
InterPro; IPR001511; ..
Pfam; PF00560; LRR: 4.
PRINTS; PR00019; LEURICHRPT.
                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                   [2]
SEQUENCE FROM N.A.
STRAIN-COLUMBIA;
PubMed-10907853;
                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                         NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Receptor.
SEQUENCE
                                               Q9LI76;
                              971760
RESULT
Q9LI76
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InterPro;
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013228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa, Arthropoda, Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera, Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

TISSUE-TAIL MUSCLE, HINDLIMB MUSCLE;

TISSUE-TAIL MUSCLE, Atkinson B.G.;

"Expression of the Myosin Heavy Chain Genes in the Tail Muscle of Thyroid Hormone-induced Metamorphosing Rana catesbelana Tadpoles.";

Dev. Genet. 0:0-0(1999).

EMBL; AF097907; AAD13772.1; -.

InterPro; IPR000533; -.

InterPro; IPR002928; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rana catesbelana (Bull frog).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 31; DB 13; Length 826; 100.0%; Pred. No. 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  826 AA; 95361 MW; 8F9E3B0579D0F483 CRC64;
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                                                                                                                                                                                                                                                                                                                         01-WAY-1999 (TrEMBLrel. 10, Created)
01-WAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          856 AA.
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01-MAY-2000 (TrEMBLrel. 13, Last sequ
01-JUN-2000 (TrEMBLrel. 14, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF01576; Myosin_tail; 1. PRINTS; PR00194; TROPOMYOSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                            MYOSIN HEAVY CHAIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                               104 LASNLES 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=8400;
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                                  1 LASNLES 7
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SEQUENCE
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RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

Ra de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

Bodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkow B.C., Dunn P.,

Ra Durbin K.J., Evangelista C.C., Ferrac S., Fleischmann W.,

RA Cosler C., Gabriellan A.E., Garrell J.H., Gu Z., Guan P., Harris M.,

Ra Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

Ra Hostin D., Houston K.A., Howland T.J., Wei M.-H., Degwam C.,

RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Jalali M., Malush F., Karpen G.H., Ke Z., Kennison D., Lia Z.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Martulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

RA Palazzolo M., Pittuan G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Syirskas R., Rassarman D.A., Weinstock G.M., Weissenbach J.,

RA Shirskas R., Rassarman D.A., Weinstock G.M., Weissenbach J.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,

RA Zheng X.H., Moors E.W., Rubin G.M., Venter J.C.;

RA Globs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RA Sheng X.H., Moors E.W., Rubin G.M., Venter J.C.;

RA Globs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RA Sheng X.H., Moors E.W., Rubin G.M., Venter J.C.;

RA Globs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RE Schence 287:2195(2000).

RE PERELL, Moors E.W., Rubin G.M., Venter J.C.;

RE Schence 287:2195(2000).
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-MAR-2011 (TrEMBLrel. 16, Last annotation update)
MYOSIN HEAVY CHAIN.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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85.7%; Pred. No. 1.2e+02;
Live 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000048; ...
InterPro; IPR001609; ...
InterPro; IPR001609; ...
Pfam; PF00612; IQ; I.
Pfam; PF00612; IQ; I.
Pfam; PF00612; IQ; I.
Pram; PF001576; MyoSin_tail; I.
PRINTS; PR00193; MYOSINHEAVY.
SWART; SM00015; IQ; I.
SWART; SM00015; IQ; I.
SQUENCE 1939 AA; 223178 WW; 4D4E3E037B7550E9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SECUENCE FROM N.A.
STRAIN=WHITE LEGHORN; TISSUE=PECTORALIS MUSCLE;
Chao T.H., Bandman E., Moore L.;
Submitted (FEB-1977) to the EMBL/GenBank/DDBJ databases.
EMBL; U87231; AB47555.1; -
HSSP; P08799; 1MMD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    856 AA; 93777 MW; 3B6C3F8ODFEA12B7 CRC64;
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Best Local Similarity 85.77
Matches 6; Conservative
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845 IASNLES 851
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Query Match
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                                                                                                                                                                                                                                                                  TISSUE-HEART;
Machida S., Matsuoka R., Noda S., Hiratsuka E., Takagaki Y., Oana S.,
Furutani Y., Nakajima H., Takao A., Momma K.;
"Evidence for the expression of neonatal skeletal myosin heavy chain
in primary myocardium and cardiac conduction tissue in the developing chick heart.";
                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                       Gaps
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               93.5%; Score 29; DB 13; Length 1939; 85.7%; Pred. No. 2.8e+02; 1ve 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1939;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                             Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases. EMBL, AB021180; BAA89233.1; -- HSSP; P08799; 1LVK. InterPro; IPR000048; -- InterPro; IPR0000533; -- InterPro; IPR000533; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OAAC40D61A2D07F3 CRC64;
                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
SKELETAL MYOSIN HEAVY CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
FAST MYOSIN HEATY CHAIN ISOFORM 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 29; DB 13;
Pred. No. 2.8e+02;
                                                                                                                               PRT; 1939 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001609; ...
InterPro; IPR002928; ...
Pfam; PF00063; myosin_head; 1.
Pfam; PF01576; Myosin_tail; 1.
PRINTS; PR00193; MYOSINHEAVY
PRINTS; PR00194; TROPOMYOSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93.5%;
  Query Match
Best Local Similarity 85.7°,
5. Conservative
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                                                                                                                              PRELIMINARY;
                                                                                                                                                                                           Gallus gallus (Chicken).
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Best Local Similarity
Matches 6; Conserv
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                                                                           1234 LASNMES 1240
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                                                                                                                                                                                                                                   NCBI_TaxID=9031;
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                                                       1 LASNLES 7
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Q9DGM4
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Milson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Wilson R., Ainscough R., Canderson K., Copsey T., Cooper J., Coulson A.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Momurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
                                                                                                                                                                                                                                                                                                                   Gaps
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01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
FAST MYOSIN HEAVY CHAIN ISOFORM 2.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

Zhang Q., Bandman E.;
Zhang Q., Bandman E.;
Seven skeletal myosin heavy chain genes (MyHC) are organized as a multigene complex in the chicken genome.";
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AF272033; AAF99314.1;
SEQUENCE 1944 AA; 223211 MW; 154F438220072D68 CRC64;
"Seven skeletal myosin heavy chain genes (MyHC) are organized as multigene complex in the chicken genome.";
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL: AR272034; AAF99315.1; ...
SEQUENCE 1941 AA; 223162 MW; 9C8597CICCFIDEEC CRC64;
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                                                                                                                                                                                                                                         Score 29; DB 13; Length 1941;
Pred. No. 2.8e+02;
1; Mismatches 0; Indels (
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2001 (TrEMBLrel. 16, Last annotation update)
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
SIMILARITY TO C. ELEGANS HYUPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 1944 AA
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MEDLINE-94150718: PubMed-7906398;
                                                                                                                                                                                                                                         93.5%;
85.7%;
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Matches 6; Conservative
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                     1236 LASNMES 1242
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|1239 LASNMES 1245
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Magnoliophyta, eudicotyledons, core eudicots, Asteridae, euasterids I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                      Gaps
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.; "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=ATCC 35405;
STRAIN=ATCC 35405;
STRAIN=ATCC 35405;
STRAIN=Ly., Bergaph H.L.;
"Sequences of the tapl, flgD, flgE, orf4, motA, motB, fliL, fliM, fliY, and fliP Treponema denticola genes.";
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
BMBL; AR12909; AAD20623.1; -.
InterPro; IPR00172; -.
InterPro; IPR001543; -.
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                                                                                                                                                                                                                                                   90.3%; Score 28; DB 5; Length 367; illarity 85.7%; Pred. No. 88; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90.3%; Score 28; DB 2; Length 393; 85.7%; Pred. No. 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                         Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; 050191, AAA91241.1; -
InterPro; IPR003406; -
Pfam; PF02485; Branch; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE 393 AA; 41701 MW; EF9B924DCC2AA342 CRC64;
                                                                                                                                                                                                        367 AA; 43010 MW; 72CB4A155DD447D4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
NCBL_TaxID=158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
PUTATIVE AMINOTERRASE.
Capsicum chinense.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                   393 AA.
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1; Mismatches
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PRINTS; PR00956; FLGMOTORFLIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 90.3
Best Local Similarity 85.7
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                              Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Treponema denticola.
                                                                                                                                                                                                                                                                    Best_Local Similarity
Matches 6; Conserv
                                                                                              SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
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| 1:|||||||
| 54 LSSNLES 60
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| 76 LSSNLES 82
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                                                                                                                                                                                                                                                                                                                    1 LASNLES 7
                                                                                                                            Favello T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Flagella.
                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                      Query Match
                                                elegans.
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HINDLIMB TO ACKINSON B.G.
"Expression of the Myosin Heavy Chain Genes in the Tail Muscle of
Thyroid Hormone-induced Metamorphosing Rana catesbeiana Tadpoles.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rana catesbeiana (Bull frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
                                                                                                                                                     Aluru M., Curry J., O'Connell M.A.; "Nucleotide sequence of a probable aminotransferase from habanero
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90.3%; Score 28; DB 10; Length 459; 85.7%; Pred. No. 1.1e+02; 1ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                               Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                         EMBL; AF085149; AAC78480.1; -.
HSSP; P04181; 20AT.
InterPro; 1PR0000954; -.
Pfam; PF00202; aminotran_3; 1.
PR0STTE; PS00600; AA_TRANSFER_CLASS_3; UNKNOWN_1.
Transferase; Aminotransferase.
SEQUENCE 459 AA; 50729 WW; 02ABB4D728B524E4 CRC64;
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SEQUENCE 708 AA; 81823 MW; BE2D01700017BC4C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
MYOSIN HEAVY CHAIN (FRAGMENT).
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01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
MYOSIN HEAVY CHAIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           708 AA.
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EMBL; AF097905; AAD13770.1; -
InterPro; IPR000533; -
InterPro; IPR002928; -
Pfam; PF01576; Myosin_tail; 1.
PRINTS; PR00194; TROPOWYOSIN.
Solanales; Solanaceae; Capsicum.
NCBI_TaxID=80379;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Conservative
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Matches 6; Conserv
                                                                                          SEQUENCE FROM N.A.
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200 LANNLES 206
                                                                                                                              STRAIN-HABANERO;
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4 LASNLEN 10
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Q9YHD8
ID Q9YHD8
AC Q9YHD8;
DT 01-MAY-
DT 01-MAY-
DT 01-MAY-
DE MYOSIN
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Query Match
Best Local Similarity
Matches 6; Conserv
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Touzel J.;
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64 LASNFES 70
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NON_TER
SEQUENCE
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Q95055;
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MEDLINE-99397451: Pubmed=10470850;
Kaneko T., Katch T., Sato S., Nakamura Y., Asamizu E., Kotani H.,
Miyajima N., Tabata S.;
Structural analysis of Arabidopsis thaliana chromosome 5. IX.
Squence features of the regions of 1,011,550 bp covered by seventeen pl and TAC clones...
DNA Res. 6:183-195(1999).
ENBL: AB018118; BAB09589.1; -.
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                                                            SEQUENCE FROM N.A.
TISSUE-TAIL MUSCLE, HINDLIMB MUSCLE;
Hu H., Merrifield P., Atkinson B.G.;
"Expression of the Myosin Heavy Chain Genes in the Tail Muscle of Thyroid Hormone-induced Metamorphosing Rana catesbeiana Tadpoles.";
                                                                                                                                                                                                                                                                                                                                                        09FHH2;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
101 KDA HEAT SHOCK PROTEIN, HSP101-LIKE PROTEIN.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantee; Embryophyta; Tracheophyta; Spermatophyta;
Bussicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
        Rana catesbelana (Bull frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
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                                                                                                                                                                                                                              Length 879;
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85.7%; Pred. No. 2.5e+02;
ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                 NON_TER 1 1 1 SEQUENCE 879 AA; 101710 MW; 1C456851E968A3D8 CRC64;
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Last sequence update)
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85.7%; Pred. No. 2.2e+02;
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                                                                                                                                                                                                                                                 1; Mismatches
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                                                                                                                  Dev. Genet. 0:0-0(1999).
EMBL; AF09'904; AAD13769.1; -.
InterPro; IPR000533; -.
InterPro; IPR002928; -.
Pfam; PF01576; Myosin.tail; 1.
PRINTS; PR00194; TROPOMYOSIN.
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095054;
01-FEB-1997 (TrEMBLrel, 02,
01-FEB-1997 (TrEMBLrel, 02,
                                                                                                                                                                                                                                     Best_Local Similarity 85.7
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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Best Local Similarity
Matches 6; Conserv
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                                          NCBI_TaxID-8400;
                                                                                                                                                                                                                                                                                171 LASNLEN 177
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095054
ID 095054
AC 095054;
DT 01-FEB
DT 01-FEB
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Q9FHH2
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Viscogliosi E., Durienx I., Delgado-Viscogliosi P., Bayle D., Dive D.;
"Phylogenetic implication of iron-containing superoxide dismutase
genes from trinchomonad species."

Mol. Biochem. Parasitol. 80:209-214(1996).

-I- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS (BY SIMILARITY).

-I- CATALYITC ACTIVITY: 2 PEROXIDE RADICAL + 2 H(+) = O(2) + H(2)O(2).

-I- COFACTOR: COPPER AND ZING OR IRON OF MANGANESE.

-I- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
                                                                                                                                                                                                          SECUENCE FROM N.A.
STRAIN-ATCC 30001;
Viscogliosi E., Durieux I., Delgado-Viscogliosi P., Bayle D., Dive D.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
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Viscogliosi E., Durieux I., Delgado-Viscogliosi P., Bayle D., Dive D.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                              Touzel J.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
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125 AA; 13826 MW; 108A018B073F60DD CRC64;
                                                                                        Trichomonas vaginalis.
Eukaryota; Parabasalidea; Trichomonadida; Trichomonas.
NCBI_TaxID=5722;
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Eukaryota; Parabasalidea; Trichomonadida; Trichomonas.
NCBI_TaxID=5722;
01-WAR-2001 (TrEMBLrel. 16, Last annotation update) IRON SUPEROXIDE DISMUTASE (EC.1.15.1.1) (FRAGMENT).
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01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
IRON SUPEROXIDE DISMUTASE (EC 1.15.1.1) (FRAGMENT).
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Pred. No. 51;
0; Mismatches
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MEDLINE=97047378; PubMed=8892298;
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85.7%;
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HSSP; P09157; 11SC.
InterPro; IPR001189; --
Pfam; PF00081; sodfe; 1.
Oxidoreductase.
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RX MEDLINE-ATCC 30001;
RX MEDLINE-STO43738; Pubmed=8892298;
RA Viscogliosi E., Durieux I., Delgado-Viscogliosi P., Bayle D., Dive D.;
RT "Phylogenetic implication of iron-containing superoxide dismutase
RT genes from trichomonad species.";
Mol. Biochem. Parasitol. 80.209-214(1996).
CC --- CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS (BY SIMILARITY).
CC --- CATALYTIY: 2 PEROXIDE RADICALS HICH ARE
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CC --- CATALYTIY: 2 PEROXIDE AND SINC OR IRON ON MANGANESE.
CC --- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
CC FAMILY.
CR FAMILY.
CR FAMILY.
DR HSSP; P09157; LISC.
FT NON TER 125 125
SEQUENCE 125 AA; 13776 MW; 12CCEBCB433B80DD CRC64;
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Search completed: June 28, 2001, 16:08:27 Job time: 955 sec

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0; Gaps

87.1%; Score 27; DB 5; Length 125; 85.7%; Pred. No. 51; tive 0; Mismatches 1; Indels

Query Match
Best Local Similarity 85.73
Matches 6; Conservative

1 LASNLES 7 | 1 | 1 | 1 | 1 | 64 LASNEES 70

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein · protein search, using sw model

June 28, 2001, 16:14:39 ; Search time 362.28 Seconds (without alignments) 1.506 Million cell updates/sec Run on:

US-09-724-406-32 50 Title: Perfect score:

1 QHSGELPFT 9 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

412676 seqs, 60623988 residues Searched:

412676 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

// SIDSB/gcgdata/geneseq/geneseqp/AA1980.DAT:\*
/ SIDSB/gcgdata/geneseq/geneseqp/AA1981.DAT:\*
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/ SIDSB/gcgdata/geneseq/geneseqp/AA1991.DAT:\* A\_Geneseq\_0601:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Description                      | Humanised antibody | Murine 206 antihod | Mouse antibody light | Light chain variah | Anti-human dn39 MA | HIMBO ORFX ORFO | Mouse antibody light | GM-CSF recentor al | Humanised VI, regio | Murine Fd79 antibo | Humanised Fd79 ant |
|----------------------------------|--------------------|--------------------|----------------------|--------------------|--------------------|-----------------|----------------------|--------------------|---------------------|--------------------|--------------------|
| ID                               | AAR85242           | AAR85236           | AAR75480             | AAR15440           | AAW03723           | AAB42441        | AAR75475             | AAR85176           | AAR25721            | AAB69661           | AAB69662           |
| 80                               | 17                 | 17                 | 16                   | 12                 | 17                 | 21              | 16                   | 16                 | 13                  | 22                 | 22                 |
| %<br>Query<br>Natch Length DB ID | 111                | 111                | 6                    | 125                | 132                | 405             | 6                    | 21                 | 111                 | 111                | 111                |
| &<br>Query<br>Match              | 84.0               | 84.0               | 80.0                 | 80.0               | 80.0               | 78.0            | 74.0                 | 74.0               | 74.0                | 74.0               | 74.0               |
| Score                            | 42                 | 42                 | 40                   | 40                 | 40                 | 39              | 37                   | 37                 | 37                  | 37                 | 37                 |
| Result<br>No.                    | П                  | 7                  | Э                    | ₹                  | ഗ                  | 9               | 7                    | 80                 | 6                   | 10                 | 11                 |

| Mouse antibody FB3<br>Mouse antibody F4-<br>H. Dvlori HSP60-bi | Light chain variab<br>H. pylori HSP60-bi | Porphyrin antibody | Human prostate can<br>Zebrafish PTH3R re | Human CHD1 protein | CHD1     | Amino acid sequenc | DNA encoding a pol | Human ORFX ORF949 | Human nucleic acid | Human ORFX ORF1983 | Ikaros protein SEQ | Ikaros protein SEQ | Ikaros protein SEQ | PRDI-BF1 protein z | Anti-HCV antibody | Human secreted pro | secreted | secreted | œ        | Human ORFX ORF2394 | Human cell cycle r | Human cancer assoc | Human REST protein |          |          | Amino acid sequenc | Ikaros protein. N | Ikaros isoform. U | Human Ikaros prote |
|--|--|--------------------|--|--------------------|----------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|----------|----------|----------|--------------------|--------------------|--------------------|--------------------|----------|----------|--------------------|-------------------|-------------------|--------------------|
| AAR75457<br>AAR75459<br>AAB10000                               | AAR60528<br>AAB10019                     | AAR52659           | AAK56601<br>AAY90231                     | AAY29918           | AAY29917 | AAY93276           | AAY93298           | AAB41185          | AAB21040           | AAB42219           | AAW72687           | AAW72688           | AAW72689           | AAB12076           | AAR69534          | AAB39077           | AAB39073 | AAB39071 | AAB63193 | AAB42630           | AAY44360           | AAB43935           | AAR99364           | AAR99369 | AAY43899 | AAY43900           | AAR92020          | AAW72677          | AAW70969           |
| 16<br>16<br>21   | 15<br>21                                 | 15                 | 21                                       | 20                 | 20       | 51                 | 21                 | 21                | 21                 | 21                 | 19                 | 19                 | 19                 | 21                 | 16                | 21                 | 21       | 21       | 21       | 21                 | 21                 | 21                 | 17                 | 17       | 21       | 21                 | 17                | 19                | 19                 |
| 218<br>218<br>9  | 111                                      | 212                | 523                                      | 640                | 648      | 307                | 307                | 312               | 539                | 782                | 26                 | 26                 | 26                 | 84                 | 93                | 112                | 136      | 137      | 179      | 197                | 197                | 219                | 252                | 308      | 318      | 318                | m                 | 334               | 334                |
| 74.0<br>74.0<br>72.0   | 72.0                                     |                    | 72.0                                     | 72.0               | 72.0     | 70.0               | 70.0               | 70.0              | 70.C               | 70.c               |                    |                    |                    |                    |                   |                    |          | ж        | ж        | 8                  | æ                  | æ                  | 68.0               | ω.       | 68.0     | ω,                 | œ                 | œ                 | 0.89               |
| 37<br>37<br>36   | 36                                       | 36                 | 36                                       | 36                 | 36       | 32                 | 35                 | 32                | 32                 | 32                 | 34                 | 34                 | 34                 | 34                 | 34                | 34                 | 34       | 34       | 34       | 34                 | 34                 | 34                 | 34                 | 34       | 34       | 34                 | 34.               | 34                | 34                 |
| 12<br>13<br>14   | 15<br>16                                 | 17                 | 16                                       | 20                 | 21       | 22                 | 23                 | 24                | 25                 | 56                 | 27                 | 28                 | 53                 | 30                 | 31                | 32                 | 33       | 34       | 35       | 36                 | 37                 | 38                 | 39                 | 40       | 41       | 42                 | 43                | 44                | 45                 |

### ALIGNMENTS

Antibody; varicella zoster virus; Ab; VSV; treatment; prevention; infection; detection; isolation; monoclonal antibody; MAb; mimetic; humanised; murine; heavy chain; light chain; variable region; CDR; Humanised antibody variable light chain region (VZV HuVK). AAR85242 standard; Protein; 111 AA. 09-APR-1996 (first entry) NEWM; REI. AAR85242; AAR85242 

Synthetic.

W09531546-A1

23-NOV-1995.

95WO-US05305. 28-APR-1995;

94US-0234133. 28-APR-1994;

(SCOT-) SCOTGEN BIOPHARMACEUTICALS INC.

Wallace TP; Moss MT, Carr FJ, Harris WJ,

WPI; 1996-010932,01.

Varicella zoster virus gpIII antibody with humanised variable region - for treatment, prevention or diagnosis of varicella zoster virus infections

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Synthetic.
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                                                                                                                                                                         binding to a varicella zoster virus (VZV) can be used to treat or prevent VZV infection. They may optionally be attached to a therapeutic agent. They may also be used, when labelled, to detect VZV particles and infected cells in blood; for the removal.

Convertablisation of infections VZV in blood; for the selection.

Considerion of human monoclonal Abs and for the design of (non-) peptide mimetics with similar diagnostic and therapeutic uses. The contral period of provider is design of the portion is derived from murine Ab 206 and the neavy and light chain variable region frameworks are NEWM and REI caspectively. The framework may include at least one mutation that improves binding specificity or affinity. The heavy and light chain cariable regions are preferably (VZVUH-VH, -VHKFIIS, -VHTLY, -VHKVRSE or -VHS) and VZVHUVK respectively.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Varicella zoster virus gpIII antibody with humanised variable region - for treatment, prevention or diagnosis of varicella zoster virus infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                     Antibodies (Ab) comprising a humanised variable region specifically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
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Pred. No. 0.29;
0; Mismatches 1; Indels
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                                              Claim 7; Page 31; 58pp; English.
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/label= CDR 1.
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Peptides AAR75462-92 are examples of complementarity determining regions (CDRs) used to generate antibodies against immunorecessive antigens.
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                                                                                     princing to a varicella zoster virus (VZV) can be used to treat or prevent VZV infection. They may also be used, when labelled, to detect VZV particles and infected cells in blood: for the removal/ variation of infectious VZV in blood: for the selection/ isolation of human monoclonal Abs and for the design of (non-) peptide minetics with similar diagnostic and therapeutic uses: The variable region CDR portion is derived from murine Ab 206 and the heavy and light chain variable region frameworks are NEWM and REI respectively. The framework may include at least one mutation that improves binding specificity or affinity. The heavy and light chain variable regions are preferably (VZVHu-VH, -VHKVRSE or -VHS) and VZVHUVK respectively.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                               variable region specifically
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse antibody light chain variable region CDR3 peptide #11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 42; DB 17; Length 111; Pred. No. 0.29; 0; Mismatches 1; Indels
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                                                                   Antibodies (Ab) comprising a humanised
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR75480 standard; Peptide; 9 AA.
Claim 2; Figure 2; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84.0%;
88.9%;
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93US-0164022.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-FEB-1996 (first entry)
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Best Local Similarity 88.9
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                111 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QHSGELPFT 9.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9515982-A2
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08-DEC-1993;
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The CDRs are derived from the heavy and light chain variable regions of the antibodies PB3-2 (AAQ92500-1), F4-7 (AAQ9502-3) and H3-3 (AAQ92504-5). The peptides AAR75470-81 represent CDR3 from the light chain variable regions. The CDR sequences were isolated from a variegated display library (VDL) of variable regions derived from a repertoire of antibodies from an immunotolerised animal. The VDL is generated by PCR amplifying the variable regions from the antibody coding sequences using the primers AAQ74153-74. The constructed antibodies are on a foetal, cancer or stem cell, which can differentiate between variant the AACP4161 variable regions from a foetal, cancer or stem cell, which can differentiate between variant of the antigen. The antibodies generated can be used in
                                                                                                                                                                                                                                                                                                                                              the diagnosis, e.g. detection of the immunorecessive antigen, or in therapy e.g. of cancer, Alzheimer's disease or familial hypercholesterolaemia. The method of production of the antibody allows rapid and sensitive isolation of antibodies that would be difficult to isolate by standard methods. The antibodies produced have greater binding affinity than those produced by combinatorial/hybridoma methods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 AA;
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; 0 Score 40; DB 16; Length 9; Pred. No. 3.4e+05; 1; Mismatches 1; Indels 80.08; 77.88; Query Match 80.0 Best Local Similarity 77.8 Matches 7; Conservative 1 QHSGELPFT 9 1 ghsweipft 9 ð

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Gaps

Light chain variable region of MAb 2C2. AAR15440 standard; Protein; 125 AA. (first entry) 25-FEB-1992 AAR15440; RESULT AAR15440 

HRV; ICAM-1; antigen-binding fragment; inflammation; auto-immune disease.

Homo sapiens

EP459577-A.

04 - DEC - 1991.

91EP-0201243. 25-MAY-1991;

90US-0532001.

01-JUN-1990;

(MERI ) MERCK & CO INC.

Tomassini JE, Sardana VV; Condra JH, Colonno RJ,

WPI; 1991-355850/49.

Microbially expressed portions of monoclonal antibody - can attachment of rhinovirus ligands to inter-cellular adhesion molecule (ICAM-1)

can block

Claim 1; Page 20; 28pp; English.

This is one of six antibody fragments from Mab's specific for domain 1 of ICAM-1. The peptide fragments can be used to treat or prevent rhinovirus infection. See AAR15437-R15443.

125 AA; Sequence 80.0%; Score 40; DB 12; Length 125;

Query Match

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Monoclonal antibodies specific for different epitope(s) on human gp39 - used for inhibiting B cell activation and for the diagnosis of various disorders, e.g. cancer, psoriasis etc..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is the light chain variable region of the murine anti-human glycoprotein (gp) 39 monoclonal antibody (MAb) 39-17 (a member of the murine kappa II subfamily). The MAb was prepd. by immunisting a 6-8 week old BALD/C mouse with a gp39-CD8 fusion protein, and 3 days later harvesting and fusing spleen and lymph cells to mouse melanoma cells, to produce an anti-human gp39 MAAb producing hybridoma. The MAb may be useful for diagnosing disease states, inhibiting B-cell activation and for treating immunological disorders, e.g. autoimmune disorders, allergic responses, organ rejection and graft versus sp39 on their surface, e.g. tumour cells, and to target therapeutic agents to such cells.
                                                                                                                                                                                                                                                                  Light chain; variable region; murine; mouse; anti-human; disease; glycoprotein 39; gp39; monoclonal; antibody; 39-1.7; hybridoma; diagnosis; inhibition; B-cell; activation; treatment; disorder; immune; autoimmune; allergic response; organ rejection; drug; graft versus host; cell imaging; tumour; targetted; delivery;
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                       Indels
                                                                                                                                                                                                                                        Anti-human gp39 MAb 39-1.7 light chain variable region.
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                     ί,
       0.85;
77.8%; Pred. wc.
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Hollenbaugh D, Siadak AW;
                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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/label= mat_peptide
                                                                                                                                                   AAW03723 standard; Protein; 132 AA.
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 Best Local Similarity 77.8
Matches 7; Conservative
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93 qhsweipft 101
                                                1 QHSGELPFT 9
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                                                                                                                                                                                                                                                                                                                                                targeted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antiparkinsonian; nootropic; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     open reading frame; ORFX; detection; cytostatic; hepatotropic;
The MAD inhibits the CD40/gp39 interaction, therefore limiting both pyfim. and sec. responses to T-cell dependent antigens and Ab prodn. specific to these antigens. A typical compsn. for intramuscular injection pref. contains 50 mg of MAD in 1 ml of sterile buffered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel nucleic acids and peptides derived from open reading frame X,
                                                                                                                                                                                                             0;
                                                                                                                                                                       80.0%; Score 40; DB 17; Length 132; 77.8%; Pred. No. 0.91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease
                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human ORFX ORF2205 polypeptide sequence SEQ ID NO:4410.
                                                                                                                                                                                                               1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                       AAB42441 standard; Protein; 405 AA.
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99US-0127636.
99US-0127728.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                           Best Local Similarity 77.8
Matches 7; Conservative
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                                                                                                                                                                                                                                                                        132 AA;
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                                                                                                                                                                                                                                                1 QHSGELPFT 9
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                                                                                                                    Sequence
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Peptides AAR75462-92 are examples of complementarity determining regions (CDRs) used to generate antibodies against immunorecessive antigens.
            immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiloflammatory; antibacterial; antiviral; antifungal; antitheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The
                                                                                                                            nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Primer; amplification; PCR; mouse; kappa chain; heavy chain; Fab; antibody; immunotolerance; animal; variegated display library; CDR; variable region; antigen; immunorecessive; cell surface marker; foetal; cancer; stem cell; variant; therapy; Alzheimer's disease; hybridoma; familial hypercholesterolaemia; binding affinity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Generating new antibodies specific for immunorecessive epitopes by selection from variegated V gene library cloned from immuno:tolerance derived antibody repertoire, useful in diagnosis,
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osteopathic; anticonvulsant; antiarthritic; immunosuppressant;
                                                                                                                                                                                                                                                                                                                                                                                                              78.0%; Score 39; DB 21; Length 405; 87.5%; Pred. No. 5.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Barsomian G, Copeland DP, Hillhouse D, Johnson T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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Best Local Similarity 87.5
ابت 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                         405 AA;
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AAR75475
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The peptide is derived from CDR III of the recombinant antibody light chain analogue of GM-CSF, 23.2.

21 AA;

Sequence

22 X 8

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Gaps

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The CDRs are derived from the heavy and light chain variable regions of the antibodies FB3-2 (AAQ92500-1), F4-7 (AAQ92502-3) and H3-3 (AAQ92500-5). The peptides AAR75470-81 represent CDR3 from the light chain variable regions. The CDR sequences were isolated from a repertoir of antibodies from a immunotolerised animal. The VDL is generated by PCR amplifying the variable regions from the antibody coding sequences using the primers AAQ74153-74. The constructed antibodies are generated against an immunorecessive antigen e.g. a cell surface marker on a foetal, cancer or stem cell, which can differentiate between variant or related forms of the antigon. The antibodies generated can be used in the diagnosis, e.g. eq. detection of the immunorecessive antigen, or in
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                                                                                                                                                                                                    therapy e.g. of cancer, Alzheimer's disease or familial hypercholesterolaemia. The method of production of the antibody allows rapid and sensitive isolation of antibodies that would be difficult to isolate by standard methods. The antibodies produced have greater binding affinity than those produced by combinatorial/hybridoma methods.
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                                                                                                                                                                                                                                                                                                                                                           Score 37; DB 16; Length 9;
Pred. No. 3.4e+05;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alpha-chain; GM-CSF; receptor; granulocyte; macrophage; colony stimulating factor; binding assay; antagonist; inflammation; autoimmune disease; agonist; upregulator; immune system cell; CDR III; light chain; antibody 23.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GM-CSF receptor alpha-chain binding peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR85176 standard; peptide; 21 AA.
                                                                                                                                                                                                                                                                                                                                                         74.0%;
66.7%;
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Matches 6; Conserv
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immunoglobulin; CDR; HSV; non immunogenic; herpes simplex
                                                                                                                                                                                                                                                                                   virus; HSV; light chain; variable region; framework; human; Pom.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New immunoglobulin(s) having murine CDRs in human framework regions - have lower antigenicity; useful for treating e.g. HSV. CMV, T-cell disorders, myeloid disorders and auto-immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence shows the humanised mature light chain variable region of the mouse Fd79 antibody. Murine CDRs were used in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schneider WP;
Score 37; DB 16; Length 21;
Pred. No. 0.5;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                       Humanised VL region of the mouse Fd79 antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Landolfi NF, Queen CL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "mutated residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "mutated residue"
                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                      AAR25721 standard; Protein; 111 AA.
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/note= "CDR"
                                                                                                                                                                                                                                                                                                                                                                "CDR"
                                                                                                                                                                                                                                                                                                                                                                                              "CDR"
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                                                                                                                                                                                                             13-JAN-1993 (first entry)
             Best Local Similarity 77.8
Matches 7; Conservative
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/note=
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2 qhsrelpwt 10
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                                                     1 QHSGELPFT 9
                                                                                                                                                                                                                                                                                                               Mus musculus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-DEC-1991;
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  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                            Region
                                                                                                                                         AAR25721
                                                       δ
                                                                                                                                                                    The present peptide binds the alpha-chain of the GM-CSF receptor, and can therefore be used in binding assays in place of GM-CSF. It can also be used as an antagonist, i.e. in the treatment of inflammation or autoimmune diseases, or in the prodn. of GM-CSF agonists, i.e. upregulators for the prodn. of immune system cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying biologically active protein peptide mimics - by prepn. of recombinant antibody libraries and synthesising complementary determining region sequences.
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Weiner DB,

Kieber-Emmons T, Von Feldt JM,

WPI; 1995-392919/50.

(UYPE-) UNIV PENNSYLVANIA.

(WIST-) WISTAR INST

95WO-US05160.

26-APR-1995; 29-APR-1994;

WO9529690-A1

39-NOV-1995

Claim 13; Page 49; 70pp; English.

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Gaps

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22; Length 111; 1; Indels

Score 37; DB : Pred. No. 3.1; 2; Mismatches

74.08;

Query Match Best Local Similarity هه ۲۰۰۰ درم و G; Conservative

1 QHSGELPFT 9

111 AA;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Humanised immunoglobulin; mouse; human; antibody; heavy chain; diabetes; light chain; graft versus host disease; transplant; autchimmune disease; multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus; myasthenia gravis; herpes infection; myeloid leukaemia; CMV infection.
human Pom framework to produce a pure humanised immunoglobulin (Ig) which is capable of binding to a herpes simplex virus-specific epitope. The Ig is non immunogenic, due to the human framework, and has a strong affinity for its predetermined antigen. They can be produced in large quantities via recombinant DNA and monoclonal antibody technology. The humanised Igs may be used alone or in combination with chemotherapeutic agents such as non-steroidal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         containing DNA segments encoding humanized heavy and light chain
variable regions, and expressing the DNA segments in the cell
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Pred. No. 3.1;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Murine Fd79 antibody light chain SEQ ID NO: 46.
                                                                                                                          anti-inflammatory drugs or immunosuppressants.
See also AAR25722-32.
                                                                                                                                                                                                                                                                                                                                                                                                                           AAB69661 standard; Protein; 111 AA
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89US-0310252.
90US-0590274.
90US-0634278.
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66.7%;
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                                                                                                                                                                                                                                                 Best Local Similarity 66.7
Matches 6; Conservative
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93 qhsweipyt 101
                                                                                                                                                                                 Sequence 111 AA;
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13-FEB-1989;
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                                                                                                                                                                                                                Humanised immunoglobulin; mouse; human; antibody; heavy chain; diabetes; light chain; graft versus host disease; transplant; autoimmune disease; multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus; myasthenia gravis; herpes infection; myeloid leukaemia; CWV infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Producing humanized immunoglobulin, involves producing a cell containing DNA segments encoding humanized heavy and light chain variable regions, and expressing the DNA segments in the cell -
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                                                                                                                                                                                 Humanised Fd79 antibody light chain SEQ ID NO: 47
                                                                                 AAB69662 standard; Protein; 111 AA.
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89US-0310252.
90US-0590274.
90US-0634278.
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                                                                                                                                                 (first entry)
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 93 qhsweipyt 101
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28-SEP-1990;
19-DEC-1990;
                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                                 30-APR-2001
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                                                                                                                    AAB69662;
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93 qhsweipyt 101

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Primer; ampiffication; PCR; mouse; kappa chain; heavy chain; Fab; antibody; irmunotolerance; animal; variegated display library; variable region; antigen; immunorecessive; cell surface marker; foetal; cancer; sten cell; variant; therapy; Alzheimer's disease; hybridoma; familial hypercholesterolaemia; binding affinity.
                                                                            Mouse antibody FB3-2 light chain variable region protein sequence.
                                                                                                                                                                                                                                                                                                                                                                       Generating new antibodies specific for immunorecessive epitopes by selection from variegated V gene library cloned from immuno:tolerance derived antibody repertoire, useful in diagnosis,
                                                                                                                                                                                                                                                                                                                      Copeland DP, Hillhouse D, Johnson T;
                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 76-77; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                            purifcn. and therapy, e.g. of cancer
          AAR75457 standard; Protein; 218 AA.
                                                                                                                                                                                                                                       94WO-US14106.
                                                                                                                                                                                                                                                             94US-0350400
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                                                     07-FEB-1996 (first entry)
                                                                                                                                                                                                                                                                                              (GENZ ) GENZYME CORP.
                                                                                                                                                                                                                                                                                                                                          WPI; 1995-224291/29.
                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAQ92501
                                                                                                                                                                     Mus musculus.
                                                                                                                                                                                                                                                                                                                  Barsomian G,
                                                                                                                                                                                                                                     08-DEC-1994;
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                                                                                                                                                                                                                                                             06-DEC-1994;
                                                                                                                                                                                                                                                                        08-DEC-1993;
                                                                                                                                                                                                               15-JUN-1995
                                 AAR75457;
AAR75457
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The sequence of the light chain variable region from the mouse antibody FB3-2. This sequence was isolated from a variegated display library (VDL) of variable regions derived from a repertoire of antibodies from an immunotolerised animal. The VDL is generated by PCR amplifying the variable regions from the antibody coding sequences using the primers AAQ74153-74. The variable regions, esp the complementarity determining regions (CDR; see AAR75462-93 for examples of CDRs) from the immunotolerant animals' antibodies are used to construct an antibody against a immunorecessive antigen e.g. a cell surface marker on a foetal, cancer or stem cell, which can differentiate between variant or related forms of the antigen. The antibodies generated can be used in the diagnosis, e.g. detection of the immunorecessive antigen, or in therapy e.g. of cancer, Alzheimer's disease or familial hypercholesterolaemia. The method of production of the immunorecessive antigen, or in therapy e.g. of cancer, Alzheimer's disease or familial hypercholesterolaemia. The method of production of the antibody allows rapid and sensitive isolation of antibodies that would be difficult to isolate by standard methods. The antibodies produced have greater binding affinity than
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Sequence

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Gaps
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 74.0%; Score 37; DB 16; Length 218; 66.7%; Pred. No. 6.6; 1; Mismatches 1; Indels
                                     1; Indels
                                     Conservative
Query Match
Best Local Similarity
Matches 6; Conserv
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Gaps

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1; Indels

2; Mismatches

Score 37; DB 16; Length 218; Pred. No. 6.6;

74.0%; 66.7%;

Best Local Similarity 66.7 Matches 6; Conservative

Query Match

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RESULT 14

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93 qhsweipyt 101 1 QHSGELPFT 9 ð

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The sequence of the light chain variable region from the mouse antibody F4-7. This sequence was isolated from a variegated display library (VDL) of variable regions derived from a repertoire of antibodies from an immunotolerised animal. The VDL is generated by PCR amplifying the variable regions from the antibody coding sequences using the primers AAQ7413-74. The variable regions, esp the complementarity determining regions (CDR; see AAR5462-93 for examples of CDRs) from the immunotolerant animals' antibodies are used to construct an antibody against a immunorecessive antigen e.g. a cell surface marker on a foetal, cancer or stem cell, which can differentiate between variant or related forms of the antigen. The antibodies generated can be used in the diagnosis, e.g. detection of the immunorecessive antigen, or in therapy consumptions of antibodies generated and sensitive isolation of antibodies that would be difficult to isolate by standard the cancer of the antibodies that would be difficult to isolate by standard the cancer of the immunorecessive by cancer of the immunorecessive antigen of antibodies that would be difficult to isolate by standard the cancer of the immunorecessive antigen affinity than
                                                                                                                                                                                    Primer; amplification; PCR; mouse; kappa chain; heavy chain; Fab; antibody; immunotolerance; animal; variegated display library; variable region; antigen; immunorecessive; cell surface marker; foetal; cancer; stem cell; variant; therapy, Alzheimer's disease; hybridoma; familial hypercholesterolaemia; binding affinity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    by selection from variegated V gene library cloned from immuno:tolerance derived antibody repertoire, useful in diagnosis, purifcn. and therapy, e.g. of cancer
                                                                                                                                              Mouse antibody F4-7 light chain variable region protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Generating new antibodies specific for immunorecessive epitopes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Copeland DP, Hillhouse D, Johnson T;
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               AAR75459 standard; Protein; 218 AA.
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                                                                                                   07-FEB-1996 (first entry)
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                                                                                                                                                                                                                                                                                                                       Mus musculus.
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                                                            AAR75459;
AAR75459
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Secretion sequence; vector; antibody; single chain antibody; promoter; Bacillus subtilis; ss.

Light chain variable region of monoclonal antibody 5E8.

07-APR-1995 (first entry)

AAR60528;

AAR60528 standard; Protein; 111 AA.

AAR60528

Tortora O, Tosi C;

Cuzzoni A, De FERRA F, Grandi G,

(ENIE ) ENIRICERCHE SPA.

94EP-0200564. 93IT-0MI0456.

05-MAR-1994; 10-MAR-1993;

14-SEP-1994. EP614982-A. Synthetic.

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This invention describes a novel method for the detection of a mammalian infection by an acid-resistant microorganism (A) by treating a faecal sample with at least two different monoclonal antibodies (MAD) (or their fragments or derivatives) or aptamers (collectively (I)) and detecting formation of a complex (C) between (I) and the corresponding antigen of formation of a complex (C) between (I) and the corresponding antigen of (A). The first and second (I) bind to epitopes of different antigens. (A). These epitopes are present, after passage through the intestines, in at least some mammals, and have either: (i) their native structure; or (ii) a structure against which an antibody is produced by an animal infected or immunized with (A), or its extract, lysate, derived protein or fragment, or with a synthetic peptide. Practically all mammals display at least one of the specified epitopes. The method is used to detect infection by acid-fast bacteria, particularly of the genera Helicobacter, Mycobacterium and Campylobacter, specifically H. pylori, H. hepaticus, confinementically. The method is direct and non-invasive, and provides an inexpensive and easily standardizable diagnosis, despite possible degradation of antigens during passage through the intestines. This sequence represents a fragment of a H. pylori heat shock protein, RSP60-binding antibody light chain complementarity determining region CDR3 which is used to illustrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Detecting infection by acid-fast microbes for diagnosis of Helicobacter pylori, comprises reacting a faecal sample with two binding reagents for antigens that survive intestinal passage
                                                                                                                                                                                                                                                                                                                                    Acid-resistant microorganism; detection; faecal; intestine; infection; monoclonal antibody; heat shock protein; HSP60; light chain; CDR; complementarity determining region.
                                                                                                                                                                                                                                                                     H. pylori HSP60-binding antibody light chain CDR3 protein fragment.
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                                           AAB10000 standard; Protein; 9 AA.
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98EP-0120687
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                                                                                                                                                                                              01-NOV-2000 (first entry)
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Best Local Similarity 77.0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-365747/31.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200026671-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-OCT-1999;
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06-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ringeis A;
                                                                                                                      AAB10000;
AAB10000

AAB10000

AAB10000

XX AAB1

XX AAB1
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The sequence encoding the variable region of the light chain of the monoclonal antibody 5EB (specific for the alpha subunit of human gonaddrophin) was amplified for its use in a recombinant vector which also comprised (1) the promoter of the gene for the neutral protease of Bacillus subtilis EGSC 1A341, (2) the secretion sequence described in AAQ17278. The amplified fragment was used to produce a DNA sequence encoding an antibody in single molecule form with the sequence VH/VK-L-VK/VH-(TAG)n, where VH and VK are the variable regions of the heavy and light chains of the antibody and List she crecognised by polyclonal light chains of the antibody and List she recognised by polyclonal antibodies directed towards the same peptide n is 1 or 0. The vector is used for the production of single chain antibodies which have improved pharmacokinetic properties and can be production of antibodies in completely soluble form with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                            subtilis - contg. neutral protease promoter and specific leader sequence, providing high yield of soluble antibody for diagnostic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72.0%; Score 36; DB 15; Length 111; 77.8%; Pred. No. 5.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Vector for secretion of single chain antibody from Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
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Job time: 1327 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 3; Figure 2; 27pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or therapeutic use
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qhsrelplt:101
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Gaps

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Score 36; DB 21; Length 9; Pred. No. 3.4e+05; 0; Mismatches 2; Indels

72.0%; 77.8%;

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RESULT 15

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Sequence 40, Appl
Sequence 2, Appli
Sequence 2, Appli
Sequence 46, Appl
Sequence 47, Appl
Sequence 47, Appl
Sequence 47, Appl
Sequence 46, Appl
Sequence 46, Appl
Sequence 46, Appl
Sequence 46, Appl
                                                                         June 28, 2001, 16:01:15 ; Search time 138.34 Seconds (without alignments) 1.311 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 46, Appl
Sequence 16, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
                                                                                                                                                                                                                                                                                                                                                                                                /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
              Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCT - US95 - 0516 - 2

US - 07 - 634 - 278 - 46

US - 07 - 634 - 278 - 46

US - 08 - 477 - 728 - 47

US - 08 - 477 - 728 - 47

US - 08 - 477 - 728 - 47

US - 08 - 474 - 040 - 46

US - 08 - 487 - 200 - 47

US - 08 - 487 - 200 - 47

US - 08 - 487 - 500 - 47

US - 08 - 484 - 537 - 47

PCT - US94 - 14106 - 57

S206152 - 7

US - 08 - 570 - 227 A - 6

US - 09 - 077 - 991 - 8

US - 09 - 262 - 773 - 2
                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCT-US94-14106-40
US-08-712-212-2
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GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
                                                                                                                                                                                                                              193259 seqs, 20144635 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                               OM protein – protein search, using sw model
                                                                                                                                                                                                       Gapop 10.0 , Gapext 0.5
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                                                                                                                             US-09-724-406-32
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Maximum DB seq length: 2000000000
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880.0
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APPLICANT: Sladak, Anthony W.
APPLICANT: Hollenbaugh, Diane L.
APPLICANT: Hollenbaugh, Diane L.
APPLICANT: Goldon, Marcia L.
APPLICANT: Goldon, Marcia L.
APPLICANT: Bajorath, Jurgen
APPLICANT: Antifo, Alejandro A.
TITLE OF INVENTION: Monoclonal Antibodies Specific For
TITLE OF INVENTION: Different Epitopes of Human gp39 and Methods For Their Use
NUMBER OF SEQUENCES: 57
                                                                        Sequence 62, Appl
Sequence 62, Appl
Sequence 12, Appl
Sequence 201, Appl
Sequence 4, Appl 1
Sequence 4, Appl 1
Sequence 199, Appl 2
Sequence 195, Appl 2
Sequence 197, Appl 3
Sequence 197, Appl 3
Sequence 197, Appl 3
Sequence 197, Appl 3
Sequence 196, Appl 3
Sequence 197, Appl 3
Sequence 196, Appl 3
Sequence 196, Appl 3
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       Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Description of the sequence Descr
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Sequence 1
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US-08-570-227A-4
US-09-077-991-6
US-09-075-991-6
US-08-399-411-62
US-08-516-859A-62
US-08-08-347-12
VS-US-08-11-417C-201
US-08-711-417C-199
US-08-711-417C-199
US-08-711-417C-195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/14106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 46, Application PC/TUS9414106
; Sequence Afo. Application PC/TUS9414106
; GENERAL INFORMATION:
; APPLICANT:
TITLE OF INVENTION: Process for Get
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BE PC COMPATIBLE
COMPUTER: IB PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 16, Application US/08379057; Patent No. 5876950; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 77.8*;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6
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1 QHSWEIPFT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCT-US94-14106-46
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US-08-379-057-16
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  228
332
332
337
337
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Sequence 6, Appli Sequence 8, Appli Sequence 4, Appli Sequence 2, Appli Sequence 186, App Sequence 186, App Sequence 187, App

US-08-711-417C-186 US-08-711-417C-187 US-08-711-417C-188 US-08-711-417C-189

Sequence 189,

46, APP1 47, APP1 47, APP1 47, APP1 47, APP1 47, APP1 53, APP1 57, APP1 57, APP1 6, APP1 6, APP1 6, APP1 6, APP1 6, APP1 6, APP1

Sequence 4 Sequence 4 Sequence 5 Sequence 5 Patent No.

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COMPUTER READABLE FORM.
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/14106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ó
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 74.0%; Score 37; DB 5; Length 9; Best Local Similarity 66.7%; Pred. No. 1.4e+05; Matches 6; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/379,057
FILING DATE: 26-JAN-1995
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: POOR: Brian W.
REGISTRATION NUMBER: 32,928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
              ADDRESSEE: Bristol-Myers Squibb Company STREET: 3005 First Avenue
                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 0N0133-
TELEPHONE: (206) 727-3670
TELEPHONE: (206) 727-3601
INPORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 132 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 40, Application PC/TUS9414106 GENERAL INFORMATION:
                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80.0%;
77.8%;
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FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
PCT-US94-14106-40
                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
CORRESPONDENCE ADDRESS:
                                                           CITY: Seattle
STATE: Washington
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                                                                                                   USA
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PCT-US94-14106-40
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                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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Query Match

74.0%; Score 37; DB 2; Length 21;
Best Local Similarity 77.8%; Pred. No. 0.24;
Matches 7; Conservative 1; Mismatches 1; Indels
                                                                                       GENERAL INFORMATION:
APPLICANT: Williams, William V.
APPLICANT: Kiebber-Emmons, Thomas
APPLICANT: Weiner, David B.
APPLICANT: VonFeldt, Joan M.
TITLE OF INVENTION: Biologically active peptides and
TITLE OF INVENTION: methods of identifying the same
NUMBER OF SOUDENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSE: Woodcock Washburn Kurtz Mackiewicz &
ADDRESSE: No. 5837460ris
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Kieber-Emmons, Thomas
APPLICANT: Weiner, David B.
APPLICANT: VonFeldt, Joan M.
TITLE OF INVENTION: Biologically active peptides and
TITLE OF INVENTION: methods of identifying the same
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: USA

ZIP: 19103
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BATCH COMPATIBLE
COMPUTER: TOWN COMPATIBLE
FILING DATE: 03-5EP-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/235,404
FILING DATE: 23-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UPN-1554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application PC/TUS9505160 GENERAL INFORMATION:
APPLICANT: Williams, William V.
                                          ; Sequence 2, Application US/08712212; Patent No. 5837460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: UP TELECOMMUNICATION INFORMATION: TELEPHONE: 215-568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , MOLECULE TYPE: protein US-08-712-212-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
RESULT 4
US-08-712-212-2
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CORRESPONDENCE ADDRESS:

1 QHSGELPFT 9

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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: QUEEN, Cary L.
APPLICANT: CO. Man Sung
APPLICANT: CO. Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: 379 Lytton Avenue CITY: Palo Alto STATE: California
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 210.2010
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
                    ADDRESSEE: Norris
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05160
                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/235,404
FILING DATE: 29-APR-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: UPN-2245
TELECOMMUNICATION INFORMATION:
TELECHONE: 215-568-3439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 46, Application US/07634278
Patent No. 5530101
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: protein PCT-US95-05160-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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                                                                                                         USA
                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                             19103
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                                                                                                      COUNTRY:
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                                                                                  STATE:
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Gaps
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Pred. No. 1.5;
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Patent No. 5530101
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: CO, Man Sung
APPLICANT: COENTEIDER, William P.
APPLICANT: COENTEIDER, William P.
APPLICANT: COENTEIDER, Nathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: PAPLICATION NUMBER: US/07/634,278 FILING DATE: 19-DEC-1990 CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74.0%; Scor.
66.7%; Pred. No. 1.-
2; Mismatches
                                                                                                                                                                                                                                                                           11823-002600
PRIOR APPLICATION DATA.

APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-5EP-1990
PRIOR APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY AGENT INFORMATION:
NAME: Smith, William M REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002601
TELEFANG (415) 326-2400
TELEFANG (415) 326-2400
TELEFANG (415) 326-2402
TELEFANG (415) 326-2422
TENDRAMICATION INFORMATION:
TELEFANG (415) 326-2400
TELEFANG (415) 326-2400
TELEFANG (415) 326-2402
TELEFANG CHARACTER STOLES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 66:/*;
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 111 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear; MOLECULE TYPE: peptide US-07-634-278-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: US
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93 QHSWEIPYT 1.01
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US-07-634-278-47
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ADDRESSEE:
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                                                 LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 11823-002600 TELECOMMUNICATION: INFORMATION: TELEPHONE: (415) 326-2400 TELEFAX: (415) 326-2422 INFORMATION FOR SEQ ID NO: 46:
                                                                                                                                                                              11823-002600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/477,728
CLASSIPICATION: 124
CLASSIPICATION: 124
CLASSIPICATION: 124
PRIOR APPLICATION: 0474
APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAMME: SMITH MAILIAM MARKE: SMITH, WAILIAM MARKE: SMITH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 46, Application US/08477728 Patent No. 5585089 GENERAL INFORMATION:
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823
TELECPHONE: (415) 326-2400
TELEPHONE: (415) 326-2422
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 66./۳
اتات 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , MOLECULE TYPE: peptide US-07-634-278-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Palo Altó
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ||| |:|:|
93 QHSWEIPYT 101
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94111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-477-728-46
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Gaps
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Query Match

24.0%; Score 37; DB 1; Length 111;
Best Local Similarity 66.7%; Pred. No. 1.5;
Matches 6; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Harold E.
APPLICANT: SELICK, HAROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF INVENTION: 113
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OURTRAILUS SYSTEM:
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
O7-JUN-1995
CLASSITCATION:
APPLICATION NUMBER:
FILING DATE:
O7-JUN-1995
CLASSITCATION:
APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
O7/590,274
FILING DATE:
APPLICATION NUMBER:
APPLICAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Townsend and Townsend and Crew LLP Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11823-002600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
BEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 47, Application US/08477728 Patent No. 5585089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 11:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 47:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
                          4: 111 amino acids amino acid
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , MOLECULE TYPE: peptide US-08-477-728-47
                                                                                                                             single
                                                                                                                                                                                                , MOLECULE TYPE: peptide US-08-477-728-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: Two Embarc
CITY: Palo Alto
STATE: California
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                                                                                                                                                                     linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93 QHSWEIPYT 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QHSGELPFT 9
                                                                                                                    STRANDEDNESS:
TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RY: US
94111
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RESULT 11
US-08-474-040-47
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                                                                                             RESULT 10
US-08-474-040-46
Sequence 46, Application US/08474040
Fatent No. 5693761
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, William P.
APPLICANT: LANDOLFI, William P.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND Khourie and Crew
STREET: 379 Lyton Avenue
CITY: Palo Alto
STATE: California
COUMTRY: US
      Score 37; DB 1; Length 111;
Pred. No. 1.5;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74.0%; Score 37; DB 1; Length 111; 66.7%; Pred. No. 1.5; Live 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATUS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RAPPLICATION NUMBER: US/08/474,040
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
    74.0%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-242
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity 60.7.
Fra 6; Conservative
Query Match
Best Local Similarity 66.7
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                               1 QHSGELPFT 9
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Sequence 47, Application US/08474040
Patent No. 5693761
GENERAL INFORMATION:
APPLICANT: OUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: COLNEIDER, William P.
APPLICANT: COLINGLE, Nicholas F.
APPLICANT: SCHINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INFURINON: IMPROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,040
FILING DATE: 07-JUN 1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/534,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 13-EEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/390,975
FILING DATE: 12-EEP-1989
ATTORNEY/AGENT INFORMATION:
NAME: SMICH, MILLIAM M
REGISTRATION NUMBER: 11823-002600
TELECOMMUNICATION INMBER: 11823-002600
TELECOMMUNICATION INMBER: 11823-002600
                                                                                                                                                                                                                                                                                Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 46, Application US/08487200; Patent No. 5693762; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 47:
                                                                                                                                                                                                                                                                                            STREET: 379 Lytton Avenue CITY: Palo Alto
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best_Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-474-040-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93 OHSWEIPYT 101
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                                                                                                                                                                                                                                                                                                                                                                                                94301
                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
US-08-487-200-46
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Pred. No. 1.5;
2; Mismatches 1; Indels
                   APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,200
CLASSIPPTAMETE: 7-JUN-1995
                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: 379 Lytton Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11823-002610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-198
ATTORNEY/AGENT INFORMATION:
NAME: SMITH MAILIAM M
NAME: SMITH WAILIAM M
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 47, Application US/08487200
Patent No. 5693762
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, NICHOLAS F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 46:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74.08;
66.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
QUEEN, Cary L.
                                                                                                                                                        113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 74.0
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: peptide US-08-487-200-46
                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                  Palo Alto
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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                                                                                                                                                                                                                                                                                                                  ZIP: 94301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 13
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Score 37; DB 1; Length 111;
Pred. No. 1.5;
2; Mismatches 1; Indels
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Patent No. 6180370

GENERAL INCOMMATION:

APPLICANT: CO. Man Sung

APPLICANT: CO. Man Sung

APPLICANT: LANDOLFI, Nicholas F.

APPLICANT: LANDOLFI, Nicholas F.

APPLICANT: SELICK, Harold E.

TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS

NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESS:
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew
STREET: 379 Lytton Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: 379 Lytton Avenue
                                                                                                                                                                                                                                                                                              SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 11823-002610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
                                                                                                                                                                                                                                                                                                                                 CURRENT AGENTIAN DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/487,200

FILING DATE: 7-UNY-1995

CLASSIETCATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/634,278

FILING DATE: 19-DEC-1990

PRIOR APPLICATION NUMBER: US 07/590,274

FILING DATE: 18-E8P-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/310,252

FILING DATE: 13-FEB-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/290,975

FILING DATE: 28-DEC-1988

ATTORNEY/AGENT INFORMATION:

NAME: Smith, William M

REGISTATION NUMBER: 30,222

REGISTATION NUMBER: 30,222
                                                                                                                                                                                                                     COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: PATENT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74.0%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                               ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) MOLECULE TYPE: peptide US-08-487-200-47
                                                                                                                        CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93 QHSWEIPYT 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-484-537-46
                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             q
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Score 37; DB 4; Length 111; Pred. No. 1.5;
                  SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/534,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
APPLICATION NUMBER: US 07/290,975
FILING DATE: 18-DEC-1988
APPLICATION NUMBER: US 0290,975
FILING DATE: 19-DEC-1988
APPLICATION NUMBER: US 0200,975
FILING DATE: 19-DEC-1988
APPLICATION NUMBER: US 0200,975
FILING DATE: US 
                                                                                    APPLICATION NUMBER: US/08/484,537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: June 28, 2001, 16:01:15
Job time: 523 sec
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Best Local Similarity 66.7.
6, Conservative
                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: linear;
; MOLECULE TYPE: peptide
US-08-484-537-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               single
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93 QHSWEIPYT 101
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STRANDEDNESS:
                                                                                                                         FILING DATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 47, Application US/08484537
Patent No. 6180370
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO. Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: COBLINGH, Kathleen L.
APPLICANT: COBLINGH, Rathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INFORMION: IMPROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
STREET: Ablo Alto
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,537
                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY AGENT INFORMATION:
NAME: SMITCH, William NEGISTRATION NUMBER: 30,233
REFERENCE/DOCKET NUMBER: 11823-002600
TELEPHONE: (415) 326-2400
TELEPHONE: (415) 326-2402
TELEPHONE: (415) 326-2402
TELEPHONE: (415) 326-2402
TELEPHONE: (415) 326-2402
                                                                                                                                                                                                                    PC-DOS/MS-DOS
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                          COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-SOPERATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: peptide US-08-484-537-46
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ||| |:1:|
93 QHSWEIPYT 101
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                                                                     94301
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1; Indels

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GenCore version 4.5
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OM protein - protein search, using sw model

June 28, 2001, 15:58:46 ; Search time 234.85 Seconds (without alignments) 2.919 Million cell updates/sec Run on:

US-09-724-406-32 50 1 QHSGELPFT 9 Perfect score: Sequence: Title:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 segs, 76174552 residues Searched:

219241 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Listing first 45 summaries Maximum Match 100% Post-processing: Minimum Match 0%

PIR\_68:# Database :

piri:\* pir2:\* pir3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

| :        | Description  | Iq light chain V r | nder pr | hypothetical prote |        | light chai |        | kappa  |          | Q)     | finger protein ZNF |        | g kappa | inger pr | protein | protein ( |        | inger protein ( | protein ( | protein ( |        |        | finger protein (cl | oa chain | c      | +      |        | inger protein ( |        |
|----------|--------------|--------------------|---------|--------------------|--------|------------|--------|--------|----------|--------|--------------------|--------|---------|----------|---------|-----------|--------|-----------------|-----------|-----------|--------|--------|--------------------|----------|--------|--------|--------|-----------------|--------|
| <b>.</b> | ID           | PH1077             | S06576  | T42663             | T16387 | S59640     | S09963 | A56169 | 140867   | B84431 | F43284             | KVMS75 | KVMS85  | S06562   | S06571  | S06574    | S05632 | S06580          | S06558    | S06581    | S06561 | S06555 | S00832             | S68241   | JC5810 | S06553 | S06567 | ~               | S06573 |
| 6        | DB.          | 7                  | ~       | 7                  | 7      | 7          | 7      | 7      | ~        | ~      | ~                  | -      | -       | N        | ~       | ~         | ~      | ~               | ~         | 7         | ~      | ~      | ~                  | ~        | ~      | ~      | ~      | 7               | 7      |
| 1        | Match Length | 102                | 223     | 405                | 594    | 101        | 111    | 210    | 384      | 1143   | 25                 | 111    | 111     | 112      | 138     | 140       | 157    | 169             | 196       | 196       | 196    | 196    | 214                | 218      | 218    | 247    | 252    | 280             | 336    |
| Query    | Match        |                    |         |                    |        | 74.0       |        |        |          | 74.0   |                    |        |         |          | 72.0    |           | 72.0   | 72.0            | 72.0      | 72.0      | 72.0   | 72.0   | 72.0               | 72.0     | 72.0   |        |        | 72.0            |        |
| 9        | score        | 40                 | 38      | 38                 | 39     | 37         | 37     | 37     | 37       | 37     | 36                 | 36     | 36      | 36       | 36      | 36        | 36     | 36              | 36        | 36        | 36     | 36     | 36                 | 36       | 36     | 36     | 36     | 36              | 36     |
| Result   | 2            | 1                  | 7       | ٣                  | 4      | S          | 9      | 7      | <b>œ</b> | σ,     | 10                 | 11     | 12      | 13       | 14      | 15        | 16     | 17              | 18        | 19        | 20     | 21     | 22                 | 23       | 24     | 25     | 56     | 27              | 28     |

| finger protein (cl<br>nitrogen regulatio | nitrogen regulation hypothetical | finger protein XFO | finger protein (cl | finger protein XFG | gene XGF 5.1C prot | zinc finger protei | zinc finger protei | finger protein XFG | finger protein XFO | hypothetical prote | zinc-finger protei | anti-idiótypic ant |
|--|----------------------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| S06566<br>RGECGL                         | A24114<br>F86074                 | S65086             | 506556             | S32036             | 151699             | 154338             | 139200             | S32037             | S65088             | T47156             | S51037             | PL0207             |
| 77                                       | ~ ~                              | ~                  | ~                  | 7                  | ~                  | ~                  | ~                  | ~                  | ~                  | ~                  | 7                  | 7                  |
| 337                                      | 349                              | 353                | 439                | 445                | 462                | 474                | 484                | 493                | 591                | 634                | 675                | 131                |
| 72.0<br>72.0                             | 72.C<br>72.C                     | 72.0               | 72.0               | 72.0               | 72.0               | 72.0               | 72.0               | 72.0               | 72.0               | 72.0               | 72.0               | 70.0               |
| 36<br>36                                 | 36<br>36                         | 36                 | 36                 | 36                 | 36                 | 36                 | 36                 | 36                 | 36                 | 36                 | 36                 | 35                 |
| 30<br>31                                 | 33<br>33                         | 3.4                | 36                 | 37                 | 38                 | 36                 | 40                 | 41                 | 42                 | 43                 | 44                 | 45                 |

### ALIGNMENTS

|   |     | 178-0    |
|---|-----|----------|
|   |     | (clone 1 |
|   |     | region   |
|   |     | >        |
| 4 |     | chain    |
| 3 | 177 | ight     |

C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000
C; Accession: PH1077
R; Tilliman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A; Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective A; Reference number: PH0971; MUID:92381444

A;Status: nucleic acid sequence not shown A;Molecule type: mRNA A;Residues: 1-102 <TIL>

A: Experimental source: B cell, strain [NZB x NZW]F1 C; Superfamily: immunoglobulin V region; immunoglobulin homology C; Keywords: immunoglobulin F;16-94/Domain: immunoglobulin homology <IMM>

Gaps ; 0 Query Match 80.0%; Score 40; DB 2; Length 102; Best Local Similarity 77.8%; Pred. No. 0.62; Matches 7; Conservative 1; Mismatches 1; Indels

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1 OHSGELPFT 9 ŏ

93 QHSWEIPFT 101 셤

## RESULT

finger protein (clone XlcGF52-1) - African clawed frog (fragment)
C; Species: Xenopus laevis (African clawed frog)
C; Species: Xenopus laevis (African clawed frog)
C; Date: 28-Reb-1990 #sequence\_revision 28-Feb-1990 #text\_change 31-Dec-1993
C; Accession: S06576
R; Nietfeld, W.; El-Baradi, T.; Mentzel, H.; Pieler, T.; Koester, M.; Poeting, A.; Kno J. Mol. Biol. 208, 639-659, 1989
A; Title: Second-order repeats in Xenopus laevis finger proteins.
A; Reference number: S05632; MUID: 90040698
A; Accession: S06576
A; Status: not compared with conceptual translation

A; Molecule type: mRNA A; Residues: 1-223 <NIE> C; Keywords: DNA binding; zinc finger

Gaps ö Query Match 78.0%; Score 39; DB 2; Length 223; Best Local Similarity 87.5%; Pred. No. 2.3; Matches 7; Conservative 0; Mismatches 1; Indels

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2 HSGELPFT 9

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A;Cross-references: EMBL:U25122
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin homology <IMM>
F;6-64/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                          Best_Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Conservative
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Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93 OHSWEIPYT 101
A; Residues: 1-101 <BOS>
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83 QHSWEIPYT 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QHSGELPFT 9
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Amolecule type: DNA
A;Residues: 1-594 cRAV>
A;Cross-references: EMBL:U39993; NID:g1055098; PID:g1055099; PIDN:AAA81086.1; CESP:F47E1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: CESP:F47E1.3
A;Introns: 20/1; 54/3; 78/3; 104/3; 163/3; 186/3; 297/2; 352/1; 396/3; 457/1; 502/2; 541
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559640
19 light chain V region N10 - mouse (fragment)
19 light chain V region N10 - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Dectes: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 21-Jan-2000
C;Accession: 559640
N;Bossart-Whitaker, P.; Chang, C.Y.Y.; Novotny, J.; Benjamin, D.C.; Sheriff, S.
J. Mol. Biol. 283, 559-575, 1995
A;Titler The crystal structure of the antibody N10-staphylococcal nuclease complex at ;
A;Reference number: 599639; MUID:96068846
                                                                                                                                        C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Accession: T42663
C; Accession: T42663
R; Bloecker, H.; Boecher, M.; Brandt, P.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, November 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
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hypothetical protein F47E1.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T16387
B;Favello, T
Submitted to the EMBL Data Library, November 1995
A;Reference number: 218505
A;Reference number: 218505
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                                                                                                                                                                                                                                                                                                                A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-405 <AAAA.
A;Cross-references: EMBL:AL133062
A;Experimental source: adult testis; clone DKFZp434N0615
C;Genetics:
                                                                                                                      hypothetical protein DKFZp434N0615.1 - human (fragment)
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Matches 7; Conservative
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A; Accession: T42663
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Best Local Similarity
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573 QHSGEKPF 580
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     195 HSGEKPFT 202
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A:Molecule type: mRNA
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T42663
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C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 21-Jan-2000
C; Accession: S09963
E; Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jaton, J.C.; Izui, S.
Eur. J. Immunol. 20, 771-777, 1990
A; Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibo
A; Recession: S09955; MUID:90269328
A; Molecule type: mRNA
A; Residues: 1-111 <REIS
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Ig kappa chain V region (clone 23.2) - mouse (fragment)

Ig kappa chain V region (clone 23.2) - mouse (fragment)

Ig kappa chain V region (clouse mouse)

Ig have charter 19-oct-1995 #sequence_revision 19-oct-1995 #text_change 11-Jan-2000

Ig have charter 19-oct-1995 #sequence_revision 19-oct-1995 #text_change 11-Jan-2000

Ig have charter 1950 for the charter of the c
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-54/Pomain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74.0%; Score 37; DB 2; Length 111; 66.7%; Pred. No. 2.8; tive 2; Mismatches 1; Indels
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A; Residues: 1-210 <MOND
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
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      Length 101;
                                                                                                                                     Indels
74.0%; Score 37; DB 2;
66.7%; Pred. No. 2.5;
tive 2; Mismatches
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Length 52;

DB 2;

Score 36;

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72.0%;
75.0%;
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Best Local Similarity 77.8%
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Best Local Similarity 77.0.
ناب 7; Conservative
                                                                        6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: protein A; Residues: 1-111 <WEI>
                                                     Best Local Similarity
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                                                                                                                                                            21 HSGEKPYT 28
                                                                                                                      2 HSGELPFT 9
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                            Query Match
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                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable receptor protein kinase [imported] - Arabidopsis thaliana
(Species: Arabidopsis thaliana (mouse-ear cress)
(C.Species: Arabidopsis thaliana (mouse-ear cress)
(C.Species: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
(C.Saccession: B84431
(C.Y.: Kaul, X.: Kaul, S.: Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
(E.Y.: Marian, W.C.; White, O.; Eisen, J.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
(E.Y.: Mature 402, 761-768, 1999
(M. Torenson and analysis of chromosome 2 of the plant Arabidopsis thaliana.
(A. Reference number: A84420; MUID:20083487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S
                                                                 C; Accession: 140867
R:Traving, C.; Schauer, R.; Roggentin, P.
Glycoconi, J. 11, 141-151, 1994
A:Title: Gene structure of the 'large' sialidase isoenzyme from Clostridium perfringens A; Reference number: 140865, MUID:95102306
A.Accession: 140867
A.Stctus: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-384 <RES>
A; Cross-references: EMBL:X87369; NID:9853805; PIDN:CAA60797.1; PID:9853808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rilichter, P.; Bray, P.; Ried, T.; Dawid, I.B.; Ward, D.C.
Genomics 13, 999-1007, 1992
A:Title: Clustering of C2-H2 zinc finger motif sequences within telomeric and fragile
A:Reference number: A43284; WUID:92372070
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                        C; Species: Clostridium perfringens
C; Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Homo sapiens (man)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 20-Mar-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
A;Modecule type: DNA
A;Residues: 1-52 -LIC>
A;Cross-references: GB:M88361; NID:g340459; PID:g553813
A;Note: sequence extracted from NCBI backbone (NCBIN:111644, NCBIP:111646)
C;Keywords: zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                    74.0%; Score 37; DB 2; Length 384; 66.7%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
hypothetical protein 2 - Clostridium perfringens
                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   finger protein ZNF52 - human (fragment)
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Best Local Similarity
Tr Conserve
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A; Residues: 1-1143 <STO>
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Matches 6; Conserv
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157 KHIGDLPFT 165
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A;Molecule type: protein
A;Residues: 1-111 <WEI>
A;Rote: the PC4285 and PC4039 sequences are identical
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C;Superfamily: immunoylobulin V region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C;Superfamily: immunoglobulin V region; immunoglobulin homology (C;Keywords: heterotetramer; immunoglobulin neptrocetramer: immunoglobulin homology cirM> F;IG-94/Domain: immunoglobulin homology cirM> F;23-92/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                               Ig kappa chain V region (PC7175) - mouse (tentative sequence)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Dacession: 1993 #sequence_revision 30-Jun-1993 #text_change 31-Mar-2000
C;Accession: B01938; A01938
R;Welgert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A;Fitle: Rearrangement of genetic information may produce immunoglobulin diversity.
A;Reference number: A93204; MUID:79073152
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Nature 276, 785-790, 1978
A;Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A;Reference number: A;3204; MUID:79073152
A;Accession: A01939
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                                      Gaps
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Pred. No. 1.9;
                                  1; Mismatches
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77.8%;
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RESULT 14

$306571

finger protein (clone XlcGF44-2) - African clawed frog (fragment)

C;Species: Xenopus laevis (African clawed frog)

C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 10-Oct-1997

C;Accession: $06571

R;Nieffeld, W.; B1-Bazadi, T.; Mentzel, H.; Pieler, T.; Koester, M.; Poeting, A.; Knoech
A;Title: Second-order repeats in Xenopus laevis finger proteins.

A;Reference number: $05632; MUID: 90040698
finger protein (clone XlcGF49-1) - African clawed frog (fragment)

(Species: Xenopus laevis (African clawed frog)

(Species: Xenopus laevis (African clawed frog)

(Spaces 1990 #sequence_revision 28-Feb-1990 #text_change 31-Dec-1993

(SAccession: 806574

R:Nietfeld, W.; El-Baradi, T.; Mentzel, H.; Pieler, T.; Koester, M.; Poeting, A.; Knoech J. Mol. Biol. 208, 639-659, 1989

A:Title: Second-order repeats in Xenopus laevis finger proteins.

A:Reference number: 805632; MUID:90040698
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                                                                                                                                                          A;Title: Second-order repeats in Xenopus laevis finger proteins. A;Reference number: S05632; MUID:90040698
A;Recession: S06562
A;Recession: S06562
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                             Score 36; DB 2; Length 112;
Pred. No. 4.4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Superfamily: LIM metal-binding repeat homology C;Reywords: DNA binding; zinc finger F;34-93/Domain: LIM metal-binding repeat homology <LIM4>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
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C;Keywords: DNA binding; zinc finger
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Best Local Similarity 75.0%;
Matches 6; Conservative 1
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A; Residues: 1-138 <NIE>
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56 HTGEKPFT 63
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54 HIGERPFT 61
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S06574
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

June 28, 2001, 15:54:39 ; Search time 105.36 Seconds (without alignments) 2.926 Million cell updates/sec Run on:

US-09-724-406-32 50 1 QHSGELPFT 9 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

93435 seqs, 34255486 residues Searched:

93435 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SwissProt\_39:\*

# STIMMADTEC

| BS        |        | scripti      | et sudoux 727814 | Series Stim |            | 8 xeno    | xenopiis   | xenopus    | xenopus   |              | xendous   | •          | P18737 xenopus lae | xenopus    |            |            |            |            |            | xenopus 3  | _          | P06218 klebsiella | P18747 xenopus lae | P18725 xenopus lae | P18749 xenopus lae | homo sap   | P18723 xenopus lae | 095125 homo sapien | P18714 xenopus lae |            | Q13360 homo sapien | m snm      | P52740 homo sapien |            | 0116       |
|-----------|--------|--------------|------------------|-------------|------------|-----------|------------|------------|-----------|--------------|-----------|------------|--------------------|------------|------------|------------|------------|------------|------------|------------|------------|-------------------|--------------------|--------------------|--------------------|------------|--------------------|--------------------|--------------------|------------|--------------------|------------|--------------------|------------|------------|
| SUMMARIES |        | ID           | ZG52_XENLA       | KV3S MOUSE  | KV3U_MOUSE | ZG9_XENLA | 2G44_XENLA | ZG49_XENLA | ZOZ_XENLA | ZG62_XENLA   | ZG3_XENLA | ZG64_XENLA | ZG8_XENLA          | ZO26_XENLA | ZO10_XENLA | ZO20_XENLA | ZG28_XENLA | ZG46_XENLA | ZG57_XENLA | ZGZ6_XENLA | NTRB_ECOLI | NTRB_KLEPN        | ZO28_XENLA         | ZG5_XENLA          | ZO6_XENLA          | ZI4I HUMAN | ZC48 XENLA         | Z202_HUMAN         | ZGZO_XENLA         | Y441_HUMAN | Z177_HUMAN         | ZF59_MOUSE | Z132_HUMAN         | ZN26_HUMAN | KV3V_MOUSE |
|           |        | 88           | ч                | -           | -          | -         | Н          | -          | Н         | -            | -         |            | -                  | -          | -          |            | -          | -          | -          | -          | Н.         | ٦,                | ٠,                 | ٠,                 | ٠,                 | ٦,         | ۰,                 | ۰,                 | ٠,                 | н.         | ٠,                 | <b>-</b>   |                    |            | 7          |
|           |        | Match Length | 223              | 111         | 111        | 112       | 138        | 140        | 157       | 169          | 196       | 196        | 196                | 196        | 214        | 247        | 252        | 280        | 336        | 337        | 349        | 349               | 439                | 445                | 403                | 4. (       | 140                | 648<br>818         | 6/5                | 697        | 321                | 406        | 589                | 26         | 108        |
| df        | Query  | Match        | 80               | 2           | (.4        | (4        | 72.0       | CA         | (7        | 72.0         | ~ (       | ~10        | N (                | (7)        | N 1        | NI         | N (        | 71         | $\sim$     | (7)        | ~          | 71                | 0.27               | V                  | 0.77               | чc         | N C                | 0.0                | V                  | N (        | 2                  | 0          | 0                  | œ          | ന          |
|           |        | Score        | 39               | 36          | 36         | 36        | 36         | 36         | 36        | 36           | 36        | 36         | 30                 | 36         | 36         | 90         | 9 6        | 35         | 36         | 36         | 36         | 36                | 36                 | 0 0                | 900                | 9 6        | 9 (                | 9 0                | 0 0                | 9 0        | ባ የ                | Υ C        | υ,                 | 34         | 34         |
|           | Result | No.          | 7                | 7           | r          | 4         | n,         | 9          | 7         | <b>x</b> 0 ( |           | ) F        | 1 .                | 77         | T -        | T .        | 12         | 9 1        | 7,         | Ω,         | 5 6        | 0 7               | 77                 | 7 6                | 2.4                | * 6        | 3 6                | 9 6                | 7 0                | 8 6        | V (                | 200        | T (                | 3.2        | 33         |

| b homo sapien<br>O aedes aegyp<br>E mus musculu<br>D homo sapien<br>T mus musculu<br>O gallus gall<br>L homo sapien<br>D s |            |                                  |  | : Com T :                                     |                         |                                |                         |                                  |         |                    |                    |                    |                  | 0; Gaps 0;                                 |                               |                               |   |
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| 09uny5<br>P62366<br>062366<br>014929<br>0014929<br>01362<br>013682<br>013089<br>09uks7<br>P81183  |            |                                  | ENT).  | vercentat, butereostomia; Pipoldea; Pipoldea; | r T., Koester M         | er proteins.";                 |                         | Reneat                           |         |                    |                    |                    | 96 CRC64;        | ; Length 223;<br>1; Indels                 |                               |                               |   |
| MAN<br>ARE<br>JISE<br>JISE<br>JISE<br>JAN<br>AAN<br>AAN<br>AAN<br>AAN<br>AAN<br>AAN   | ALIGNMENTS | 223 AA.                          | update) ton update) 52.1 (FRAGMENT).   | achia; F                                      | i., Pieler T.,          | laevis finger                  |                         | ; 7.<br>; 8.<br>ing: Ren         | PE.     | 7 F. F.            | P.E.               | PE.                | BFA977BB6701BA96 | ore 39; DB 1<br>ed. No. 1.2;<br>Mismatches |                               | 111 AA.                       | update)<br>n update                             |
| 2232_HUMAN<br>VCP_AEDAE<br>ZF92_MOUSE<br>2169_HUMAN<br>IKAR_MOUSE<br>IKAR_HUMAN<br>ZN35_HUMAN<br>IKAR_HUMAN<br>IKAR_HUMAN<br>HELI_HUMAN<br>HELI_HUMAN   | ALIGN      | PRT;                             | 01-NOV-1990 (Rel. 16, Last sequence update) 01-FEB-1994 (Rel. 28, Last annotation update) GASTRULA ZINC FINGER PROFEIN XLCGF52.1 (FRAGM<br>Xenopus laevis (African clawed frog). Eukaryota: Metagoa Chordata Craniata. Vorto | Mesobatr                                      | 9712;<br>Gentzel H      | opus lae<br>189).              |                         | R_C2H2_1<br>R_C2H2_2<br>DNA-bind | C2H2-TY | C2H2-TY<br>C2H2-TY | C2H2-TY<br>C2H2-TY | C2H2-TY<br>C2H2-TY | ; BFA97          | Score 39;<br>Pred. No.<br>0; Mismat        |                               | PRT;                          | ed)<br>seguence update)<br>annotation updat     |
| ппппппппппппппппппппппппппппппппппппппп   |            | eate                             | st s<br>st a<br>TEIN<br>claw   | r e   | =250<br>., M            | xen<br>9(19                    | α                       | INGE                             | ;       |                    | •                  |                    | MW for           | . 58°.                                     |                               |                               | Created)<br>Last seq<br>Last ann                |
| 4417<br>4471<br>518<br>518<br>519<br>5219<br>522<br>522<br>537  |            | ANDARD;<br>16, Cr                | 16, La<br>28, La<br>GER PRO<br>frican  | ia; Anu<br>pus.                               | PubMed<br>aradi T       | eats in:<br>:639-6576.         | M.<br>22;               | ZINC_F<br>ZINC_F<br>ZINC_F       | 27      | 83<br>111          | 139                | 195<br>223<br>223  | 2554             | 78<br>87<br>vativ                          |                               | STANDARD;                     | 01, Creat<br>01, Last<br>38, Last               |
| 668866886886886886886886886886886886886   |            | ST<br>(Rel                       | (Rel.<br>(Rel.<br>(Fin<br>(Bel.)   | xero  | M.A.<br>0698;<br>E1-B   | 208<br>208<br>3065             | 12N<br>20008            | 028;<br>0157;<br>Meta            | 196     | 61                 | 17                 | 23                 | S AA             | arity                                      | 202                           | SI                            | Rel.<br>Rel.<br>Rel.                            |
| **************************************  |            | XENLA<br>7;<br>W-1990            | W-1990<br>B-1994<br>ULA ZING<br>US laev  | bia; Bal<br>odinae;<br>TaxID=8;               | NCE FROM NE=9004(       | nd-order<br>1. Biol<br>806576; | P25490;<br>Pro; IPF     | TE; PSOC<br>TE; PSSC<br>finger;  | N S S   | 2 2 2              | SNG                | NG S               | NCE 77           | imi  | HSGELPFT<br>     <br>HSGEKPFT | 40USE                         | 21-JUL-1986 (<br>21-JUL-1986 (<br>15-JUL-1999 ( |
| 888888844444446000000000000000000000000   | RESULT 1   | ZG52_<br>ZG52_<br>P1872<br>01-NO | 01-NO<br>01-FE<br>GASTR<br>Xenop<br>Eukar  | Amphi<br>Xenop<br>NCBI                        | SEQUE<br>MEDLI<br>Nietf | "Seco.<br>J. Mo                | HSSP;<br>Inter<br>Pfam: | PROSI<br>PROSI<br>Zinc-          | ZN_FI   | ZN_FI              | ZN_FI              | ZN_FII             | 30038            | Query Match<br>Best Local S<br>Matches 7   | 2 1                           | RESULT 2 KV3S_MOUSE ID KV3S_M | 21-JUI<br>21-JUI<br>15-JUI                      |
|   | RES        | AC AC                            | DE DE  | 8888  | R R R R                 | RR                             | DR DR                   | DR<br>DR<br>W                    | FT      | FI                 | FT                 | FT                 | <u> </u>         | ÖÄÄ  | Qy                            | RESI<br>KV3S<br>ID            | DI DI   |
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PIR; A01939; KVMS85.
InterPro; IPR003006; -.
Immunoglobulin v region.
DOMAIN
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
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                                                                                                                                                                  Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.; Rearrangement of genetic information may produce immunoglobulin
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COMPLEMENTARITY-DETERMINING 3.
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Pred. No. 2.3;
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FRAMEWORK 4.
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15-JUL-1999 (Rel. 38, Last annotation update)
1G KAPPA CHAIN V-III REGION PC 2485/PC 4039.
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IG KAPPA CHAIN V-III REGION PC 7175.
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Best Local Similarity 77.8
Matches 7; Conservative
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InterPro; IPR003006; -.
Pfam; PF00047; ig; 1.
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ID KV3U_MOUSE
AC P01673;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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MEDIINE=90040698; PubMed=2509712;
Nietfeld W., El-Baradi T., Mentzel H., Pieler T., Koester M.,
Poeting A., Knoechel W.;
"Second-order repeats in Xenopus laevis finger proteins.";
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MEDLINE=90040698; PubMed=2509712;
Nietfeld W., El-Baradi T., Mentzel H., Pieler T., Koester M., Poeting A., Knoechel W.;
"Second-order repeats in Xenopus laevis finger proteins.";
J. Mol. Biol. 208:639-659(1989).
PIRS. 206562.
INESP: PRO00812;
72.0%; Score 36; DB 1; Length 111; 77.8%; Pred. No. 2.3;
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Pred. No. 2.3;
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56 C2H2-TYPE.

84 C2H2-TYPE.

C2H2-TYPE.

112 C2H2-TYPE.

112 C2H2-TYPE.

112 C2H2-TYPE.
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OLNOV-1990 (Rel. 16, Last sequence update)

01-NOV-1990 (Rel. 16, Last sequence update)

01-FEB-1994 (Rel. 28, Last annotation update)

GASTRULA ZINC FINERR RPOTEIN XLOGG44.2 (FRAGMENT).
                                                                                                                                                                                                  ZG9_XENLA STANDARD; PRT; 112 AA. P18738; 01-NOV-1990 (Rel. 16, Last sequence update) 01-NOV-1994 (Rel. 28, Last annotation update) GASTRULA ZINC FINGER PROTEIN XLCGF9.1 (FRAGMENT).
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7
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PROSITE; PS00028; ZINC_FINGER_CZH2_1; 4.
PROSITE; PS50157; ZINC_FINGER_CZH2_2; 4.
Zinc-finger; Metal-binding; DNA-binding; Repeat.
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                  Pred. No. 2.3;
0; Mismatches
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75.0%;
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                                       7; Conservative
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NCBI_TaxID=8355;
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Best Local Similarity
   Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                             93 QHSRELPLT 101
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157 AA.

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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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Median W., El-Baradi T., Mentzel H., Pieler T., Koester M., Nietfeld W., El-Baradi T., Mentzel H., Pieler T., Koester M., Poeting A., Knoechal W. Rocechal W., Second-order repeats in Xenopus laevis finger proteins.";

L. J. Mol. Biol. 2081: 599-659(1989).

R. PIR, SO5332, SO5632.

R. HSSP, P08047; 1SP2.

R. InterPro: IPR009622. -

R. Pfam; PF00096, z-C2H2; 5.

R. Pfam; PF00096; z-C2H2; 5.

R. Prosite; PS00157; zINC_FINGER_C2H2_1; 4.

R. PROSITE; PS50157; zINC_FINGER_C2H2_2; 5.

W. Zinc-finger: Metal-binding; DNA-binding; Repeat.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoldea; Pipidae;
Xenopodinae; Xenopus.
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Nietfeld W., El-Baradi T., Mentzel H., Pieler T., Koester M.,
Poeting A., Knoechel W.;
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Pred. No. 3.2;
1; Mismatches 1; Indels
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"Second-order repeats in Xenopus laevis finger proteins.";
J. Mol. Biol. 206;639-659(1989).
PIR; S06580; S06580.
HSSP; P08047; 1SP2.
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01-NOV-1990 (Rel. 16, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
GASTRULA ZINC FINCER PROTEIN XLCGF62.1 (FRAGMENT).
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Pfam; PF00096; zf-C2H2; 6.
PROSITE; PS00028; zINC_FINGER_C2H2_1; 6.
PROSITE; PS50157; zINC_FINGER_C2H2_2; 6.
Zinc-finger; Metal-binding; DNA-binding; Repeat.
                                                                      NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-FB-1994 (Rel. 28, Last annotation update)
00CYTE ZINC FINCER PROTEIN XLCOFZ (FRAGMENT).
Xenopus laevis (African clawed frog).
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C2H2-TYPE.
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75.0%;
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NCBI_TaxID=8355;
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129 HTGEKPFT 136
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01-NOV-1990 (Rel. 16, Last sequence update)
01-NOV-1994 (Rel. 28, Last annotation update)
01-FEB-1994 (Rel. 28, Last annotation update)
GASTRULA ZINC FINGER PROFIEN XLOGE49.1 (FRACMENT).
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphlbia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
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Poeting A., Knoechel W.;
Second-order repeats in Xenopus laevis finger proteins.";
J. Mol. Biol. 208:639-659(1989).
PIR; S06574; S06574.
HSSP; P25490; 12NM.
InterPro; IPR00082; -.
Pfam; PF00096; zf-C2Hz; 5.
PROSITE: PS00028; zINC_FINGER_C2H2_1; 5.
PROSITE: PS50157; zINC_FINGER_C2H2_2; 5.
Zinc_finger; Metal-binding; DNA-binding; Repeat.
                                                                                                                                                                                                                                                                                                           Score 36; DB 1; Length 138; Pred. No. 2.8; 1; Mismatches 1; Indels
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Pred. No. 2.9;
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                                            Interpro; IPR000822; -.
Pfam; PF00096; zf-C2H2; 5.
PROSITE; PS00028 zINC_FINGER_C2H2_1; 5.
PROSITE; PS00028; zINC_FINGER_C2H2_2; 5.
Zinc_finger; Metal-binding; DNA-binding; Repeat.
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J. Mol. Biol. 208:639-659(1989).
PIR; S06571; S06571.
HSSP; P08047; 1SP2.
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54 HTGEKPFT 61
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28 HTGEKPFI 35
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01-NOV-1990 (Rel. 16, Last sequence update)
01-NOV-1990 (Rel. 16, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
CASTRULA ZINC FINGER PROTEIN XLCGF3.1 (FRAGMENT).
Xenopus laevis (African clawed frog).
ENKATYOLA, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia: Batrachia; Annura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus.
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MEDILINE-90040658; PubMed-2509712;
Nietfeld W., El-Baradi T., Mentzel H., Pieler T., Koester M.,
Poeting A., Knoechel W.;
                                                                                                                                                                                                                                                                                                                           "Second-order repeats "", Anopus laevis finger proteins.";
J. Mol. Biol. 208:639-659(1989).
HSP: S06558; S06558.
HSSP: P25490; LXMM.
InterPro; IPR000822; -..
Pfam; PF00096; zf-C2H2; 7.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; 7.
PROSITE; PS00128; ZINC_FINGER_C2H2_2; 7.
Zinc_finger; Metal-binding; DNA-binding; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72.0%; Score 36; DB 1; Length 196; 75.0%; Pred. No. 4.1;
                                                                                            Score 36; DB 1; Length 169; Pred. No. 3.5;
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84 HTGEKPFT 91
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01-NOV-1990 (Rel. 16, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
01-FEB-1994 (Rel. 28, Last annotation update)
CASTRULA ZINC FINCER PROTEN KLGGF8.2DB (FRAGMENT).
Xenopus laevis (African clawed frog).
Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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Nietfeld W., El-Baradi T., Mentzel H., Pieler T., Koester M.,
Poeting A., Knoechel W.;
Second-order repeats in Xenopus laevis finger proteins.";
J. Mol. Biol. 208: 639-659(1989).
R PIR; S06561; S06561.
R PIR; S06561; S06561.
R InterPro; IPR000822; -.
R PRSP; PS2490; L37M.
R PROSITE; PS00058; Z1CZFINGER_C2H2_1; 7.
R PROSITE; PS0157; ZINC_FINGER_C2H2_2; 7.
R PROSITE; PS0157; ZINC_FINGER_C2H2_2; 7.
R Zinc-finger; Metal-binding; DNA-binding; Repeat.
T NON_TER 1 2 2 2212-TYPE.
T ZN_FING 34 56 C2H2-TYPE.
01-NOV-1990 (Rel. 16, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
01-FEB-1994 (Rel. 28, Last annotation update)
Xenopus laevis (African Clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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PIR; S06581; S06581.
HSSP; P08047; 1SP2.
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Pfam; PF00096; zf-C2H2; 7.
PROSTIE; PS00028; zINC_FINGER_C2H2_1; 7.
PROSTIE; PS00157; ZINC_FINGER_C2H2_2; 7.
ZINC_finger; Metal-binding; DNA-binding; Repeat.
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MEDLINE=90040698; Pubmed=2509712;
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NCBI_TaxID=8355;
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NCBI_TaxID=8355;
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Xenopus laevis (African clawed frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                              SEQUENCE FROM N.A.
MEDLINE-8900565; PubMed-3139407;
MEDLINE-89005665; PubMed-3139407;
Moester M., Fleiler T., Poeting A., Knoechel W.;
The finger motif defines a multigene family represented in the maternal mRNA of Xenopus laevis oocytes.";
EMBO J. 7:1735-1741(1988).
HSSP; P008047; 1592.
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MEDILINE-90040658; PubMed-2509712;
Nieffeld W. El-Baradi T., Mentzel H., Pieler T., Koester M.,
Poeting A., Knoechel W.;
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J. Mol. Biol. 208:639-659(1989).
HSP: S06553; S06553.
HSSP: P08047; 1582.
InterPro; IPR000822; -.
PREM: PF00096; zf-C2H2; 8.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; 7.
PROSITE; PS00157; ZINC_FINGER_C2H2_2; 8.
Zinc_finger; Metal-binding; DNA-binding; Repeat.
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DCEEE00EDED1A5F8 CRC64;
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Pfam; PF00096; zf-C2H2; 7.
PROSITE; PS00026; zINC_FINGER_C2H2_1; 6.
PROSITE; PS00157; zINC_FINGER_C3H2_2; 7.
Zinc-finger; Metal-binding; DNA-binding; Repeat.
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      OOCYTE ZINC FINGER PROTEIN XLCOF10 (FRAGMENT).
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NCBL_TaxID=8355;
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NCBI_TaxID=8355;
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01-NOV-1990 (Rel. 16, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
01-FEB-1994 (Rel. 28, Last annotation update)
00-CYTE ZINC FINGER PROTEIN XLCOP26 (FRAGMENT).
Xenopus laevis (African clawed frog).
Xenopus laevis (African clawed frog).
Amphibia; Batrachia; Anura: Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Miletfeld W. El-Baradi T. Mentzel H., Pieler T., Koester M., Poeting A., Knoechel W.T. Mentzel H., Pieler T., Koester M., Scond-order repeats in Xenopus laevis finger proteins."; "Second-order repeats in Xenopus laevis finger proteins."; PIR: S06555: S06555. S06555. S06555. Pofen: Poeting Proteins."; Page P25490; 12MM.
InterFro: IPR000822; - Pfam: PF00096; zf-C2H2; 7. PROSITE; PS00028; zINC-FINGER_C2H2_1; 7. PROSITE; PS00129; zINC-FINGER_C2H2_2; 7. Zinc_finger; Metal-binding; DNA-binding; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72.0%; Score 36; DB 1; Length 196; 75.0%; Pred. No. 4.1; Live 1; Mismatches 1; Indels
                                                                                                                                           Length 196;
                                                                                                                                                                            1; Indels
                                                                                              22023 MW; C65153F709EDE461 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A4417A032257D595 CRC64;
                                                                                                                                             Score 36; DB 1;
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(Rel. 16, Last sequence update)
(Rel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                   196 AA.
                                                                                                                                                          Pred. No. 4.1;
                                                                                                                                                                         1; Mismatches
                C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
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C2H2-TYPE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22659 MW;
                                                                                                                                          72.0%;
75.0%;
                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                   STANDARD;
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146
174
196
196 AA;
                                                                                            196 AA;
                                                                                                                                                       Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
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| 84 HTGEKPFT 91
                                                                                                                                                                                                      2 HSGELPFT 9
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84 HTGEKPFT 91
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01-NOV-1990
01-FEB-1994
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P18739;
ZN_FING
ZN_FING
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ZN_FING
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ZO10_XENLA
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01-NOV-1990 (Rel. 16, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
01-FEB-1994 (Rel. 28, Last annotation update)
GASTRULA ZINC FINGER PROTEIN XLGGF28.1 (FRAGMENT).
Xenopus laevis (African clawed frog).
EMARYOLAS, Metascoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Annura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nietfeld W., El-Baradi T., Mentzel H., Pieler T., Koester M., Poeting A., Knoechel W.;
"Second-order repeats in Xenopus laevis finger proteins.";
J. Mol. Biol. 208:639-659(1989).
BIR: S06567; S06567.
HSSP; P08047; 1SP2.
                                                                                                                                                                                                Ouery Match 72.0%; Score 36; DB 1; Length 247; Best Local Similarity 75.0%; Pred. No. 5.1; Matches 6; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        168 C2H2-TYPE.
196 C2H2-TYPE.
247 C2H2-TYPE.
247 C76B7808F6BE09AD CRC64;
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Pfam; PF00096; 2f-C2H2; 9.
PROSITE; PS000208; 2INC_FINGER_C2H2_1; 9.
PROSITE; PS0157; ZINC_FINGER_C3H2_2; 9.
Zinc_finger; Metal-binding; DNA-binding; Repeat.
NOW_TER 6 28 C2H2-TYPE.
ZN_FING 62 84 C2H2-TYPE.
ZN_FING 90 112 C2H2-TYPE.
ZN_FING 118 140 C2H2-TYPE.
ZN_FING 118 140 C2H2-TYPE.
ZN_FING 174 196 C2H2-TYPE.
ZN_FING 174 196 C2H2-TYPE.
ZN_FING 202 224 C2H2-TYPE.
ZN_FING 174 196 C2H2-TYPE.
ZN_FING 174 196 C2H2-TYPE.
ZN_FING 202 224 C2H2-TYPE.
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C2H2-TYPE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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202
230
252
252 AA;
  146
174
225
247
247 AA;
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112 HTGEKPFT 119
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P18716;
ZN_FING
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Gaps ő Score 36; DB 1; Length 252; Pred. No. 5.2; 1; Indels 1; Mismatches 72.0%; 75.0%; Query Match Best Local Similarity 75.0.

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2 HSGELPFT 9 δŏ

|:|| ||| 28 HTGEKPFT 35 g Search completed: June 28, 2001, 15:54:40 Job time: 128 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

June 28, 2001, 16:08:27; Search time 411.58 Seconds (without alignments) 2.893 Million cell updates/sec Run on:

US-09-724-406-32 50 1 QHSGELPFT 9 Perfect score: Sequence:

**BLOSUM62** Scoring table:

425026 seqs, 132305027 residues Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL\_16:\* Database :

1: sp\_archea:\* 2: sp\_bacteria:\* 3: sp\_fungi:\*

sp\_human:\*
sp\_invertebrate:\*
sp\_mammal:\*
sp\_mhc:\* sp\_rodent:\*
sp\_unclassified:\*
sp\_vertebrate:\* sp\_organelle:\* sp\_phage:\* sp\_plant: \* 10: 12: 13: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp\_virus:\*

## SUMMARTES

|               |       | æ              |   |    | SUMMARIES |                    |
|---------------|-------|----------------|---|----|-----------|--------------------|
| Result<br>No. | Score | Query<br>Match | Query<br>Match Length DB                | DB | GI        | Description        |
|               |       | 1              | , | 1  |           |                    |
| г             | 41    | 82.0           | 556                                     | 4  | Q9UMP5    | Ogump5 homo sanien |
| 7             | 40    | 80.0           | 488                                     | 10 | Q9LGM4    | Oglam4 orvza sariv |
| m             | 39    | 78.0           | . 278                                   | 2  | 09V718    | 09v718 drosophila  |
| 7             | 39    | 78.0           | 405                                     | 4  | Q9UFB7    |                    |
| 2             | 39    | 78.0           | 571                                     | 4  | 09GZV8    | . –                |
| 9             | 39    | 78.0           | 594                                     | Ŋ  | 020537    | Caen               |
| 7             | 39    | 78.0           | 909                                     | 4  | Q9Y2D9    |                    |
| 89            | 37    | 74.0           | 181                                     | 2  | Q9W3J3    | 09w313 drosophila  |
| σ             | 37    | 74.0           | 384                                     | 7  | . 046239  |                    |
| 10            | 37    | 74.0           | 498                                     | 4  | Q9H8L4    |                    |
| 11            | 37    | 74.0           | 501                                     | Ŋ  | Q9VG72    |                    |
| 12            | 37    | 74.0           | 525                                     | 2  | 09VN56    | 09vn56 drosophila  |
| 13            | 37    | 74.0           | 532                                     | Ŋ  | 001960    | 001960 caenorhabdi |
| 14            | 37    | 74.0           | 720                                     | 9  | Q9N003    |                    |
| 15            | 37    | 74.0           | 756                                     | S  | 061362    |                    |
| 16            | 37    | 74.0           | 891                                     | 2  | 061361    |                    |
| 17            | 37    | 74.0           | 934                                     | 5  | Q9VKF1    |                    |
| 18            | 37    | 74.0           | 936                                     | s  | 09VGK1    | _                  |
| 19            | 37    | 74.0           | 962                                     | 2  | Ö61360    |                    |
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488 AA.

Q9LGM4; 01-OCT-2000 (TrEMBLrel. 15, Created)

PRELIMINARY;

Q9LGM4

RESULT Q9LGM4 ID Q9I AC Q9I DT 01-

11:11 ||| 385 QHTGERPFT 393

q δ

1 QHSGELPFT 9

| 09zps9 arabidopsis<br>015923 homo sapien<br>092669 homo sapien<br>09nqj3 homo sapien<br>09ndj3 homo sapien | Q09047 xenopus lae<br>Q9vp31 drosophila<br>Q9psml xenopus lae<br>Q91906 xenopus lae<br>Q9h5p0 homo sapien | Q13397 homo saplen<br>Q08701 xenopus lae<br>Q99592 homo saplen<br>Q9wuk6 mus musculu<br>Q9yy3 rattus norv<br>Q9y5a5 homo saplen<br>Q9ve54 drosophila | 10   | O9piu2 homo sapien<br>Q9nxd7 homo sapien<br>Q9vt48 drosophila |
|--|---|--|--|---|
| Q92PS9<br>Q15923<br>Q92669<br>Q9NQJ3<br>Q9ZH35   | Q09047<br>Q9VP31<br>Q9PSM1<br>Q91906<br>Q9H5P0  | Q1339/<br>Q06701<br>Q99592<br>Q9WUK6<br>Q9JKY3<br>Q9Y5A5   | Q9VDN4<br>Q9GRA5<br>Q09046<br>Q9NSM4<br>Q9H1B9<br>Q9UJW8 | 09P1U2<br>09NXD7<br>09VT48                                    |
| 014442   | 13 13 4   | 5 4 1 1 1 2 2 2 2 3 3 3 4 4 5 3 3 4 5 5 5 5 5 5 5 5 5 5 5  | 2 5 5 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4                  | 4 4 N   |
| 1143<br>52<br>90<br>306<br>349   | 354<br>420<br>478<br>478  | 522<br>522<br>522<br>547<br>549  | 556<br>591<br>634<br>648<br>692                          | 692<br>1001<br>1239   |
| 74.0<br>72.0<br>72.0<br>72.0   | 722.0   | 72.0<br>72.0<br>72.0<br>72.0<br>72.0   | 72.0<br>72.0<br>72.0<br>72.0<br>72.0                     | 72.0<br>72.0<br>72.0  |
| 36   | , , , , , , , , , , , , , , , , , , ,   |  |  | 36<br>36  |
| 20<br>22<br>23<br>24   | 25<br>26<br>29<br>29  | 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3  | K W W & & & & & & & & & & & & & & & & &                  | 43<br>44<br>5   |

## ALIGNMENTS

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Gaps
                                                                                                                                                  Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostoml;
Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                A Dobner 7. C., Fischer M., Groitl P.;

"Cloning of a nevel zinc finger protein.";

"Cloning of a nevel zinc finger protein.";

"Submitted (AG1-1999) to the EMBL/GenBank/DDBJ databases.

"BEMBL; AJ24555; CAB53100.1; -.

R HSSP; P08047; 1SP2.

R Pfam; PF00096; ZINC_FINGER_C2H2; 14.

R PROSITE; PS00028; ZINC_FINGER_C2H2; 14.

SMART; SM00355; ZnF_C2H2; 1.

W DNA-binding; Metal-binding; Zinc-finger.

O SEQUENCE 556 AA; 62266 MW; E9CFFE4AF7C12E90 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82.0%; Score 41; DB 4; Length 556; 77.8%; Pred. No. 4; tive 1; Mismatches 1; Indels
                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                   556 AA.
                                   PRT;
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Best Local Similarity 77.8°
Matches 7; Conservative
                                   PRELIMINARY;
                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                   AP4 PROTEIN
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RESULT
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Q9UFB7
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Annaritdes P.G., Scherer S.E., Li Pw., Hoskins R.A., Galle R.F.,
Annaritdes P.G., Scherer S.E., Li Pw., Hoskins R.A., Galle R.F.,
Annaritdes P.G., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazel R.M., Ferrandon R.C., Rogers Y.-H.C., Blazel R.M., Man K.H., Doyle G., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Barlew R.M., Basu A., Baxendale J., Barnaktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                         Oryza sativa (Rice).
Eukaryota, Viridiplantae, Embryophyta, Tracheophyta, Spermatophyta,
Magnoliophyta; Liliopsida, Poales, Poaceae, Ehrhartoldeae, Oryzeae,
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                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
clone:P0433F09.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AP002521; BAA95760.1;
EMBL; AP002539; BAA95760.1;
                                                                                                                                                                                                                                                                                                 "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
clone:P0041E11.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INTERPRO; IPR001841; -.
Pfam; PF00097; zf-C3HC4; 1.
SEQUENCE 488 AA; 53169 MW; IFBAD40A7463C323 CRC64;
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Last annotation update)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-MAR-2001 (TrEMBLrel. 16, Last annotation update) ESTS AU075348(C11252).
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Sasaki T., Matsumoto T., Yamamoto K.;
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Matches 6; Conservative
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235 HSGEMPYT 242
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                                                                                                                                                                         NCBI_TaxID=4530;
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Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
Hostin D., Houston K.A., Howland T.J., Wei M. H., Ibegwam C.,
Alalai M., Kalush F., Karpen G.H., We Z., Kenison J.A., Ketchum K.A.,
Alalai M., Kalush F., Karpen G.H., Kravitz S., Kulp D., Lai Z.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Attei B.L., McIntosh T.C., McLeod M.P., McPherson D.,
Markei B., McIntosh T.C., McLeod M.P., McShrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Merkulov G., Milshina N.V., Nosarry C., Muzny D.M., Nelson D.L.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K.B., Nixon K., Nusskern D.R., Pacled J.M.,
RA Reinert K., Saden Kriamos I., Simpson M., Skupski M.P., Smith T.,
Spier E., Spradling A.C., Stapleton M., Stropski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Stropski M.P., Smith T.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q., Ang
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q., Zheng L.,
RA Cibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RT Science 2957:1865-21957_2000).
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Pfam: PF00096; zf-C2H2; 9.
PRINTS; PR00048; ZINCFINGER.
PROSITE; PS00028; ZINCFINGER_C2H2; 7.
SMART; SM00355; ZnF_C2H2; 1.
DNA-binding; Hypothetical protein; Metal-binding; Nuclear protein;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
EMBL; AL133062; CAB61386.1; -.
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Pred. No. 4.9;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              278 AA; 32463 MW; 3D6DEJAE5D77C223 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2001 (TrEMBLrel. 16, Last annotation update)
HYPOTHETICAL 46.0 KDA PROTEIN (FRAGMENT).
DKFZP434N0615.
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Pfam; PF00096; zf-C2H2; 7.
Pfam; PS00096; zf-C2H2; 7.
SMARY; SM0055; ZnC_CH2; 1.
DNA-binding; Metal-binding; Zinc-finger.
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Best Local Similarity 87.5%;
Matches 7; Conservative (
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NON_TER
SEQUENCE 4
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                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
ISOGAÍ T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
Magatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
Ninomiya K., Iwayanagi T.;
"NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                      Gaps
                                                                                                                                                                                                            01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last senotation update)
CDNA FLJ1233 FIS, CLONE NT2RM4000202, WEAKLY SIMILAR TO ZINC FINGER
PROTEIN MOK-2 (PR-DOMAIN CONTAINING PROTEIN 14).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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"A family of novel PR-domain (PRDM) genes as candidate tumor
Query Match 78.0%; Score 39; DB 4; Length 405; Best Local Similarity 87.5%; Pred, No. 7.3; Matches 7; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 39; DB 4; Length 571;
Pred. No. 11;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-94150718; PubMed-7906398;
Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
SIMILAR TO C2H2-TYPE ZINC FINGER.
                                                                                                                                                                                     571 AA.
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                 Pred. No. 7.3;
); Mismatches
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EMBL; AF319458; AAG39635.1; -.
SEQUENCE 571 AA; 64062 MW;
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87.5%;
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Best Local Similarity
Matches 7; Conserv
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                                                                                                227 QHSGEKPF 234
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510 QHSGEKPF 517
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Nagase T., Ishikawa K., Suyama M., Kikuno R., Hirosawa M.,
Myajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
Myajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
Myajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
The complete sequences of 100 new cDNA clones from brain which code
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                       Coulson A.,
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A. Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L., Johnston B., Alsten J., Laister N., Latreille P., Lightning J., L.oyd C., Mcmurray A., Mortimore B., O'Callaghan M., Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R., Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J., Therry-Mieg J., Thomas K., Vaudin M. K., Wadepan K., Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P., L., L., L., Mallen D., Marken D., Marken D., Marken D., Marken D., Sproat J., Mohldman P., L., L., L., L., Marken D., Ma
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Waterston R.;
Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLUIAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
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Pfam; PF00096; 2f-C2H2; 4.
PRINTS; PR00048; ZINCFINGER.
PROSITE; PS00026; ZINC_FINGER_C2H2; 3.
SMART; SM00355; ZnE_C2H2; 1.
DNA-binding; Metal-binding; Nuclear protein; Zinc-finger.
SEQUENCE 594 AA; 67531 MW; 819576E08C0CB5A7 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (NOV-1.995) to the EMBL/GenBank/DDBJ databases
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Last annotation update)
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87.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 78.0 Best Local Similarity 87.5 Matches 7; Conservative
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Pfam; PF00096; zf-C2H2; 4.

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RA Adams N.D., Celniker S.E., Lip.W., Hoskins R.A., Galle R.F.,

Adams N.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,

RA GAGTER R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA GADTI J.F., Dayle C., Scherer S.E., Lip.W., Hoskins R.A., Galle R.F.,

RA Brandon R.C., Rogers Y.H.C., Blazej R.C., Champe M., Pfeiffer B.D.,

RA Abril J.F., Agbayani A., An H.J., Andrews-Frannkoch C., Baldwin D.,

RA Ballew R.W., Basu A., Baxendall J., Baytextearoglu L., Beasley E.M.,

RA Beeson K.Y., Bencs P.V., Bernan B.P., Bhandari D., Bolshakov S.,

RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Corter A., Chandra I.,

RA Cherry J.W., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Corter A., Chandra I.,

RA Bartis K.C., Busam D.A., Butler H., Cadleu E., Bolshakov S.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,

RA Hortin D., Harvey D., Heiman T.J., Herrandez T.R., Hauris M.,

RA Hortin D., Houston K.A., Howland T.J., Welfarnandez T.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Welfarnandez T.R., Houck J.,

RA Lasko P., Lei Y., Levitsky A.A., Li J.J., Li Z., Liang Y., Lin X.,

Lasko P., Lei Y., Levitsky A.A., Li J.J., Li Z., Liang Y., Lin X.,

RA Lasko P., Lei Y., Levitsky A.A., Li J.J., Li Z., Liang Y., Lia X.,

RA Lasko P., Lei Y., Levitsky A.A., Li J.J., Li Z., Liang Y., Lia X.,

RA Lasko P., Lei Y., Moyn W. Murthoy B., Murthy L., Muzny D.M., Nelson D.L.,

RA Harris B. W., Murthy B., Murthy L., Weisserhoch J.,

RA Harris B. Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith T.,

Spiers R., Speat M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Sher E., Spradling A.C., Stapleton M., Stupski M., Stub K., Smith H.O.,

RA Sher E., Spradling S.W., Robing W., Shub S., Zhu X., Smith R.,

Ra Dang S.H., Rodong F.W., Robing W., Shub S., Zhu X., Smith R.,

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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                               Gaps
                                                                                                                                                                                               ö
                                                                                                                                    Score 39; DB 4; Length 606; Pred. No. 11;
SMART; SM00355; ZnF_C2H2; 1.
DNA-binding; Metal-binding; Nuclear protein; Zinc-finger.
SEQUENCE 606 AA; 69744 MW; C066D10E179985CC CRC64;
                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                           181 AA.
                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
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EMBL; AE003443; AAF4634.1; -.
FlyBase; FBgn0030009; CG15336.
InterPro; IPR000822; -.
                                                                                                                                    Query Match 78.0%;
Best Local Similarity 87.5%;
Matches 7; Conservative
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CG15336.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
CDNA FLJ13479 FIS, CLONE PLACEI003738, WEAKLY SIMILAR TO ZINC FINGER
                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Traving C., Schauer R., Roggentin P., "Gene structure of the 'large' sialidase isoenzyme from Clostridium perfringens A99 and its relationship with other clostridial nanH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_raxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
NANH GDNE & ORF1,2,3 & 4 PRECURSOR.
Clostridium perfringens.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
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                                                                                                                           Score 37; DB 5; Length 181;
Pred. No. 7.9;
                                                                                                                                                                       0; Indels
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EMBL; X87359; CAA60797.1; -
InterPro; IPR001798; -
Pfam; PF01144; Rel.ch; 2.
                                         Zinc-finger.
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                                                                                                                                                                       4; Mismatches
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PROSITE; PS00028; ZINC_FINGER_C2H2; 3. SMART; SM00355; ZnF_C2H2; 1. DNA-binding; Metal-binding; Zinc-finger SEQUENCE 181 AA, 21222 MW; E6169EDIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glycoconj. J. 11:141-151(1994).
                                                                                                                                  74.08;
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                  Query Match
Best Local Similarity
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58 RHTGEMPFS 66
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Barndon R.C., Rogers Y.H.C., Blazel R.G., Champe M., Pfeliffer B.D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Bascendle J., Bayraktaroglu L., Beasley E.M.,
RA Besson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Busam D.A., Burler H., Cadieu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
RA Burtis K.D., Dup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,
Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann M.,
RA Goder C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu.Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Kalush F., Karpew G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kalush F., Karpew G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Lu X., Matteil B., McIntosh T.C., McLeod M.P., Inday Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobary D.M., Nelson D.L.,
RA Reiner K., Femington K., Sungern D.R., Palazolo M., Pittman G.S., Pollact F., Scheler F., Shen H.,
RA Reiner K., Sendoris R., Vergese M.G.,
Shue B., Spradling A.C., Stapleton M., Strong R.,
Shue B.C., Stapleton M., Strong R.,
Shue B.C., Stapleton M., Strong R.,
Shieb B.C., Stapleton M., Strong R.,
RA Shieb B.C., Stapleton M., Strong R.,
Raids R., Welson D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBL_TaxID=7227;
                            TISSUE-PLACENTA;

ISOGAI T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,
Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,
Arita M., Rabekura T., Ishii S., Kawai F., Hara K., Takeuchi K.,
Arita M., Rabekura T., Ishii S., Kawai Y., Saito K., Tamamoto J.,
Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.;
NDEDO human cDNA sequencing project.";
Submitted (AGG-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AK023541; BAB14602.1;
SEQUENCE 498 AA; 54872 MW; C704FCF55CCDAEIA CRC64;
                                                                                                                                                                                                                                                                           ;
0
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74.0%; Score 37; DB 4; Length 498;
Best Local Similarity 85.7%; Pred. No. 23;
Matches 6; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
U-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
CG5245 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
               SEQUENCE FROM N.A.
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13 HAGELPF 19
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,
RA Adams M.D., Celniker S.E., Holt R.A., Baburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Gutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazef R.G., Champe M., Pfeiffer B.D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Baxendale J., Bayaktaroglu L., Beasley E.M.,
RA Beson K.Y., Bennos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Busam D.A., Baller H., Cadleu E., Center A., Chandra I.,
RA Beson K.Y., Bennos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
Gertry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Disser K.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hostin D., Harwey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Mowland T.J., Wel M.-H., Ibeeyam C.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Jalali M., Matlush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Jalali M., Mattei B., McIntosh T.C., McLeod M.P., Morpherson D..,
RA Mount S.M., Mayy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Balazzolo M., Pittman G.S., Pan H., Shulson D.K., Shen H.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
She Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shule B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).

Science 287:2185-2195(2000).

HSSP; P08047; 1SP2.
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Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Pred. No. 24;
1; Mismatches 0; Indels
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00355; ZnF_C2H2; I.
DNA-binding; Metal-binding; Zinc-finger
SEQUENCE 501 Aa; 58790 MW; BBAE04740
                                                                                                                                                                                                                                                                                                                              InterPro; IPR000822; -.
Pfam; PF00096; :: C-C2H2; 15.
PROSITE; PS00028; ZINC_FINGER_C2H2; 14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel. 13, Created)
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                                                                                                                                                                                                                                                                                           FlyBase; FBgn0038047; CG5245.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74.0%;
85.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similar.ty 85.7,
6; Conservative
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Q9VN56
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Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Zheng X.H., Zhong F.N., Zhong W., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Wapers E.W., Rubin G.M., Venter J.C., The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Boffield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Ropera A., Saunders D., Shownkeen R.,
Smaldon N., Smith A., Sonnhammer E., Staden R., Sullston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Thierry-Mieg J., Wilkinson-Sproat J., Wohldman P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                           74.0%; Score 37; DB 5; Length 525; 62.5%; Pred. No. 25; tive 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P., Biewald T.;
to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                            InterPro; 197000822; -.
Pfam; PF00096; zf-C2H2; 7.
PROSITE; PS00036; znC_FRINGER_C2H2; 7.
SMART; SM00355; znF_C2H2; 7.
SMORT; SM00355; ZnF_C2H2; 7.
SEQUENCE 525 Aa; 58076 MW; 69DELAESCA739727 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
SIMILARITY TO MULTIPLE C2H2-TYPE ZINC FINGERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  532 AA.
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MEDLINE-94150718; PubMed-7906398;
                                                                                                                                                                                           HSSP; P07248; 1PAA.
FlyBase; FBgn0037275; CG14655.
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Best Local Similarity 62.5°
Matches 5; Conservative
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Submitted (MAY-1997)
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Waterston R.;
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SEQUENCE FROM N.A.
TISSUB-CEREBELLUM CORTEX;
Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
Suzuki Y., Sugano S., Hashimoto K.;
"Isolation of full-length cDNA clones from macaque brain cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                     -:- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-:- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
-:- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
-:- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
-:- SIMILARITY: AR00313; AAB93641.1; -.
-- FAMILY: PROMONES: ZARC.
-- FA
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SMART; SM00349; KRAB; 1.

DNA-binding; Hypothetical protein; Metal-binding; Zinc-finger.

Approximator 720 AA; 83922 MW; 074A7736A5903D90 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                    74.0%; Score 37; DB 5; Length 532; 75.0%; Pred. No. 25; Live 1; Mismatches 1; Indels
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Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB046644; BAB03562.1; -.
InterPro; IPR000822; -.
InterPro; IPR001909; -.
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
HYPOTHETICAL 83.9 KDA PROTEIN
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Last annotation update)
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PROSITE; PS50805; KRAB; 1.
PROSITE; PS00028; ZINC_FINGER_C2H2; 19.
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Matches 6; Conservative
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Matches 6; Conservative
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NCBI_TaxID=9541;
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113 QHMGDLPF 120
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CROL OR CROL GAMMA OR CG14938

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OS Drosophila melanogaster (Fruit fly).

C Eukaryota: Metazoa: Arthropoda: Tracheata: Hexapoda; Insecta;

CC Ephydroidea: Drosophilidae: Disophila.

OX NCBI_TaxID=7227;

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Search completed: June 28, 2001, 16:08:28 Job time: 956 sec

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